STIC Search Report
Biotech-Chem Library

USPTO

TO: James Schultz
Location: 2d18 / 2c18
Art Unit: 1635
Monday, January 30, 2006

Case Serial Number: 09/227881

From: Noble Jarrell
Location: Biotech-Chem Library
Rem 1B71
Phone: 272-2556

Noble.jarrell@uspto.gov

Search Notes

sira
Search and Information
Resources Administration

From:	Schultz, James
Sent:	Wednesday, January 18, 2006 3:12 PM
To:	STIC-Biotech/ChemLib
Subject:	Seq Search 09/227,881

Hello,
Could you please run a score over length sequence search on SEQ ID NO:34 (5271 nt long), which returns hits between 50 and 500 nt long? I need only those hits that are 100% complementary. Please run the search in the interference databases as well.

Also, could you run a standard nucleotide sequence search on the full length of SEQ ID NO: 34, ONLY in the interference databases?

Thanks,
Doug Schultz

James Douglas Schultz, PhD
Primary Examiner
AU 1635 (Biotechnology)
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
(571) 272-0763

OM nucleic - nucleic search, using sw model

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Run on: January 25, 2006, 20:57:13

Title: US-09-227-881-34
Perfect score: 5271
Sequence: 1 atctttgttcagttcacctc.............tcgggatgagccagcaagg 5271

Scoring table: IDENTITY NUC
               Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents NA:*
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8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	5271	100.0	5271	3	US-09-306-828-34	Sequence 34, Appl
2	5271	100.0	6169	3	US-08-938-669A-3	Sequence 3, Appl
3	5271	100.0	6169	3	US-09-306-828-3	Sequence 3, Appl
4	5246.4	99.5	5300	3	US-08-938-669A-1	Sequence 1, Appli
5	5246.4	99.5	5300	3	US-09-306-828-1	Sequence 1, Appli
6	5224.4	99.1	5304	3	US-08-938-669A-2	Sequence 2, Appli
7	5224.4	99.1	5304	3	US-09-306-828-2	Sequence 2, Appli
8	1804.4	34.2	2800	3	US-09-056-28A-1	Sequence 1, Appli
9	1804.4	34.2	2800	3	US-10-017-870-10	Sequence 10, Appli
10	1804.4	34.2	2800	3	US-09-952-464A-1	Sequence 1, Appli
11	227	4.3	227	3	US-09-306-828-38	Sequence 38, Appl
12	227	4.3	283	3	US-09-306-828-37	Sequence 37, Appl
13	189.8	3.6	29326	3	US-09-949-016-15356	Sequence 15356, A
14	184.6	3.5	205044	3	US-09-949-016-15851	Sequence 15851, A
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16	184.6	3.5	205044	3	US-09-949-016-15853	Sequence 15853, A
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19	184.6	3.5	223471	3	US-09-949-016-12725	Sequence 12725, A
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27	182.8	3.5	76165	3	US-09-949-016-14005	Sequence 14005, A
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43	180.6	3.4	66933	3	US-09-544-398B-11	Sequence 11, Appl
44	180.6	3.4	66933	3	US-09-543-771B-11	Sequence 11, Appl
45	180.6	3.4	72049	3	US-09-544-398B-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-306-828-34
; Sequence 34, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 34
; LENGTH: 5271
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-34,

Query Match   100.0%;   Score 5271;   DB 3;   Length 5271;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 5271;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   4681 TGCAAGACTGAAATTAGAAAAGTTCTCCCAAAGATACACAGTTGTTGTTTAAAGCTAGGGGGTG 4740

REFERENCE/DOCKET NUMBER: 07425-0034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6857
TELEFAX: 202 383-6610
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6169 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-938-669A-3

Query Match   100.0%;   Score 5271;   DB 3;   Length 6169;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 5271;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy  121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCGTGTGTCTCTTATTTTAGTGA 180
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Db 4741 AGGGGGGAAATCTGCCGCTTGGTAGGGTGCTGTC 4800

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Qy 5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160
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Db 5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160

Qy 5161 CCTGTGCACAGCCCCCACCAGCCTACGTGGCCACCTCGTCTTCTGTCTTCCCCATGAAGGGCTG 5220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5161 CCTGTGCACAGCCCCCACCAGCCTACGTGGCCACCTCGTCTTCTGTCTTCCCCATGAAGGGCTG 5220

Qy 5221 GCTCCCCAGTATATATAAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5221 GCTCCCCAGTATATATAAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
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RESULT 2
US-08-938-669A-3
; Sequence 3, Application US/08938669A
; Patent No. 6171788
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
; TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
; TITLE OF INVENTION: RELATED DISEASES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,669A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/791,154
; FILING DATE: 28-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mendelson, Elliot
; REGISTRATION NUMBER: P-42,878

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Qy   841  GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAAATCTTAAGAAACTC  900
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Db   841  GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAAATCTTAAGAAACTC  900

Qy   901  TTGAAAGATCATGAATTTAACCATTTTAAGTATAAACAAATATGCGATGCATAATCAG    960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  TTGAAAGATCATGAATTTAACCATTTTAAGTATAAACAAATATGCGATGCATAATCAG    960

Qy   961  TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020
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Db   961  TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020

Qy  1021  GGATAGTTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTTCAGAATGATC   1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGATAGTTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTTCAGAATGATC   1080

Qy  1081  TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA  1140
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Db  1081  TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA  1140

Qy  1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC  1200

Qy  1201  TGTGCAGCCCATCCGCTCCCACAGGAGCGCACGCCCTCAATTTCTGTCTTACCTACCTGTCTTAC  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  TGTGCAGCCCATCCGCTCCCACAGGAGCGCACGCCCTCAATTTCTGTCTTACCTACCTGTCTTAC  1260

Qy  1261  TACAGCCAGAAGCTCCGTGAGGGTGAGGGTGAGGGTCTGTCTTGAACTCCTGACCTTACTGTGTATGCTCTAC  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  TACAGCCAGAAGCTCCGTGAGGGTGAGGGTGAGGGTCTGTCTTGAACTCCTGACCTTACTGTGTATGCTCTAC  1320

Qy  1321  ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAAATTCTCCTGTCTCAGCCTCC  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAAATTCTCCTGTCTCAGCCTCC  1380

Qy  1381  CGCGTAGCTGGGACTACAGGCGCACGCCCGGCCTAATTTTTGTATTGTTAGTAGTAGAGATGGG  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CGCGTAGCTGGGACTACAGGCGCACGCCCGGCCTAATTTTTGTATTGTTAGTAGTAGAGATGGG  1440

Qy  1441  GTTTCACCATATATAGCCCGGCTGTCTTGAACTCCTGACCTCAGGTGATCACCACCTC  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  GTTTCACCATATATAGCCCGGCTGTCTTGAACTCCTGACCTCAGGTGATCACCACCTC  1500

Qy  1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCCGCCCGGCCAAGGGTCAGTGT  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCCGCCCGGCCAAGGGTCAGTGT  1560

Qy  1561  TTAATAAGGAATAACTTGAATGTTTACTAAACCAACAGGGAAAACAGGAAAACAGACAAAAGCTGTGA  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  TTAATAAGGAATAACTTGAATGTTTACTAAACCAACAGGGAAAACAGGAAAACAGACAAAAGCTGTGA  1620

Qy  1621  TAATTTCAGGGATTCTTGGGATGGGAATGTGCCATGGGAGGAGAGGGAGCCCTGCCTAGAGCTGCCCAGAC  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  TAATTTCAGGGATTCTTGGGATGGGAATGTGCCATGGGAGGAGAGGGAGCCCTGCCTAGAGCTGCCCAGAC  1680

Qy  1681  CACTGGTCCTCATCACTTTCTTCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTTATT  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  CACTGGTCCTCATCACTTTCTTCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTTATT  1740

Qy  1741  CACCATGCTTTGTGTAAGCCTCCACATATGTTACTGTAAATAAGAGTATACATAAAACTAG  1800
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Db  1741  CACCATGCTTTGTGTAAGCCTCCACATATGTTACTGTAAATAAGAGTATACATAAAACTAG  1800

Qy  1801  TTCCATTTGGGCGCCATCTGTGTGTATAGGGAGGAGGGGAGCCCTGCAAGCACCCGGGTCC  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  TTCCATTTGGGCGCCATCTGTGTGTATAGGGAGGAGGGGAGCCCTGCAAGCACCCGGGTCC  1860

Qy  1861  TGAAGCCCCGGCCAGAGGTTTCTTCCTCTGCCAGTGTGGGGGAGCCCTGCAAGCACCCGGGGTCC  1920
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Db  1861  TGAAGCCCCGGCCAGAGGTTTCTTCCTCTGCCAGTGTGGGGGAGCCCTGCAAGCACCCGGGGTCC  1920

Qy  1921  TGGGGTGTCCTGAGCAACCTGCCACTCGTTGTTTGTTGTTATCACTCTCTAGG       1980
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Db  1921  TGGGGTGTCCTGAGCAACCTGCCACTCGTTGTTTGTTGTTATCACTCTCTAGG       1980

Qy  1981  GACCTGTTGCTTTCTTATTTCGTGTGACTCGTTCATTCATTCCAGGCATTCATTGACAATT  2040
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Db  1981  GACCTGTTGCTTTCTTATTTCGTGTGACTCGTTCATTCATTCCAGGCATTCATTGACAATT  2040

Qy  2041  TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGTGAGCAAAGCAGTCACTGC   2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGTGAGCAAAGCAGTCACTGC   2100

Qy  2101  CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAGCAGTGCAGAGAGCAGTGCAGAGAAATTAATAGCCA  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAGCAGTGCAGAGAAGCAGTGCAGAGAAATTAATAGCCA  2160

Qy  2161  GCCAACTAAACCCAGTGCTGAAAAGGAAAGGAAATAAACCATCTTGAAGAAATTGTGCGC  2220
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Db  2161  GCCAACTAAACCCAGTGCTGAAAAGAAAATAAACCATCTTGAAGAAATTGTGCGC       2220

Qy  2221  AGCATCCCTTAACAAGGCCACCTCCCATTACAAATGCGCCCCCCCTGCCTCCCATCGTGCCCGGAGG  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  AGCATCCCTTAACAAGGCCACCTCCCATTACAAATGCGCCCCCCCTGCCTCCCATCGTGCCCGGAGG  2280

Qy  2281  CCCCCAAGCCGAGTCTTCCAAGCTCCTCCTCCATCAGTCAGCGCTGCAGTCTGCGGCCT  2340
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Db  2281  CCCCCAAGCCGAGTCTTCCAAGCTCCTCCTCCATCAGTCAGCGCTGCAGTCTGCGGCCT  2340

Qy  2341  GCCTCGCTTCCCGTGAATCGTCCGTGGTCATCTGAGCTGGCTCGAGCTCGAGACTCCTTCAGGCT  2400
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Db  2341  GCCTCGCTTCCCGTGAATCGTCCGTGGTCATCTGAGCTGGCTCGAGCTCGAGACTCCTTCAGGCT  2400

Qy  2401  CCAGAAAGAAATGGAGAGGGAAACTAGTTCAACGGAGATCTGAGGGGACCAGTGTTTC  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  CCAGAAAGAAATGGAGAGGGAAACTAGTTCAACGGAGATCTGAGGGGACCAGTGTTTC  2460

Qy  2461  CTTCAGAGGGAGAAAGGGCCTCCAGTCTCCAGTCCCAGTGAGGAGGAGGACTCGAGGGGAG  2520
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Db  2461  CTTCAGAGGGAGAAAGGGCCTCCAGTCTCCAGTCCCAGTGAGGAGGAGGACTCGAGGGGAG  2520

Qy  2521  TGGGGACGCTGGGCTGCTGGACGGTGCTGAAAAGGCAGAGAGTGAAAAGGCAAGGCTGAA  2580
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Db  2521  TGGGGACGCTGGGCTGCTGGACGGTGCTGAAAAGGCAGAGAGTGAAAAGGCAAGGCTGAA  2580

Qy  2581  GCTGCCCAGATGTTCAGTTGTGTTCAGTGTTCACCGGGGCTGGAGTTTCCGTTGCTTCCTGTGTGAGC  2640
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Db  2581  GCTGCCCAGATGTTCAGTTGTGTTCAGTGTTCACCGGGGCTGGAGTTTCCGTTGCTTCCTGTGTGAGC  2640

Qy  2641  CTTTTTATCTTTTCTTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  CTTTTTATCTTTTCTTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC  2700

Qy  2701  ATAAAGTCAGCTGTGTTAAAATTCAGGGTGTGCATGGGTCAGGAAGGCCTTTAT       2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  ATAAAGTCAGCTGTGTTAAAATTCAGGGTGTGCATGGGTCAGGAAGGCCTTTAT       2760

Qy  2761  TTAATGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACCGAAGAAGTGAC  2820
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Db  2761  TTAATGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACCGAAGAAGTGAC  2820

Qy  2821  TGGAGTCTTTTCTTCTTCATGTCTTTCGGGCAACTACTCAGCCCTGTGGTGACTTGGCTTA  2880
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Db  2821  TGGAGTCTTTTCTTCTTCATGTCTTTCGGGCAACTACTCAGCCCTGTGGTGACTTGGCTTA  2880

Qy  2881  TGCAAGACGGTCGAAAACCTTGGAATCAGAGGACTCGGTTTCTTCCCGGCCATT       2940
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Db  2881  TGCAAGACGGTCGAAAACCTTGGAATCAGAGGACTCGGTTTCTTCCCGGCCATT       2940

Qy  2941  GGTTGGCTGTGCGACCGGTGGGCAAGTCGTCTCTTCCTTCTCTTCTCCGGCCATAGTCTTCTGCT  3000
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Db  2941  GGTTGGCTGTGCGACCGGTGGGCAAGTCGTCTCTTCCTTCTCTTCTCCGGCCATAGTCTTCTGCT  3000

Qy  3001  ATAAAGACCCTTGCAGCTCCGTGTTCTGTGAACACTTCCCTGTGATTCTTCTCTGAGGGG  3060
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Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTCTCTGTGTCAACACTTCCCTGTGATTCTCTGTGAGGGGG 3060
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Qy 3421 AGTGACCTGCACGCGCAGCGGAGAGAGAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCACGCGCAGCGGAGAGAGAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCATTCAAGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db 3481 ACAGATTCATTCAAGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
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Qy 3901 TAAACAAACACCCCAGTTGTAAATGTCTCAAGTTCAGCCTTAACTGCAGAACCAATCAAAA 3960
Db 3901 TAAACAAACACCCCAGTTGTAAATGTCTCAAGTTCAGCCTTAACTGCAGAACCAATCAAAA 3960
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Qy 4021 AGTTTGAAAATATTTACTTCACAGTATTGACACATGTTGTTGGGTATTAACAACATAAAGT 4080
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Qy 4081 TGCTCAAAGGCAATCATTATTTCAAGTGCTTAAAGTACTTCTGACAGTTTTGGTATAT 4140
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Db 4141 TTATTGGCTATTGCCATTTGCTTTTGTTTTTCTCTGGGGTTATTAATGTAAAGCAG 4200
Qy 4141 TTATTGGCTATTGCCATTTGCTTTTGTTTTTCTCTGGGGTTATTAATGTAAAGCAG 4200
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Qy 4261 TGTTTTTACCACCTTCTAACTAAATTAACATTTATTCATTGCAATAGAGCCATAAA 4320
Db 4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
Qy 4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
Db 4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTTCAAAACTA 4440
Qy 4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTTCAAAACTA 4440
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Qy 4441 CTTTGAAATTAGACCTCCTGGATCTGTTGTTTTTAACATATTTAACATATTAATAAAACATGTTTAAA 4500
Db 4501 ATTTTGATATTTTGATAATCATCTTTGTTTTCCTTTGTAATCTATATTTT 4560
Qy 4501 ATTTTGATATTTTGATAATCATCTTTGTTTTCCTTTGTAATCTATATTTT 4560
Db 4561 ATATATTTGAAAAACATCTTTCTGAGAGAGTTCCCAGATTTCACCGATGAGTTCTTGG 4620
Qy 4561 ATATATTTGAAAAACATCTTTCTGAGAGAGTTCCCAGATTTCACCGATGAGTTCTTGG 4620
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Qy 4621 CATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGGTGCTGCCTGAGA 4680
Db 4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGGTG 4740
Qy 4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGGTG 4740
Db 4741 AGGGGGGAAATCTGCGCGCTTCTATAGGAAATGCTCTCTCCCCTGGAGCCTAGGGTGCTGTC 4800
Qy 4741 AGGGGGGAAATCTGCGCGCTTCTATAGGAAATGCTCTCTCCCCTGGAGCCTAGGGTGCTGTC 4800
Db 4801 CTTGTGTTCTGGCTGTGTTATTTTCTCGTCCCTGCCTACGTCTTAAAGGACTTGTTT 4860
Qy 4801 CTTGTGTTCTGGCTGTGTTATTTTCTCGTCCCTGCCTACGTCTTAAAGGACTTGTTT 4860
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Db 5101 CAAACAGACTTCTGGAAGTTATTTTCTAAGAATCTTGCTCGGCAGCGTGAAGGCAACCCC 5160
Qy 5101 CAAACAGACTTCTGGAAGTTATTTTCTAAGAATCTTGCTCGGCAGCGTGAAGGCAACCCC 5160
Db 5161 CCTGTGCACAGCCCCAGCCTGGCCACCTGTCTTCCCCATGAAGGGCTG 5220
Qy 5161 CCTGTGCACAGCCCCAGCCTGGCCACCTGTCTTCCCCATGAAGGGCTG 5220

RESULT 3
US-09-306-828-3
; Sequence 3, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 3
; LENGTH: 6169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-3

Query Match   100.0%; Score 5271; DB 3; Length 6169;
Best Local Similarity 100.0%;
Matches 5271; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy      1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAAATAACCAATGTGAAAG   60
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Qy    121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTTATTTAGTTGA   180
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Db    121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTTATTTAGTTGA   180

Qy    181 CAGATGTTGCTCTGACAGAAGCTATTCTTCAGAAGCTATTCTTCAGAAGTCCAATATCGTAAATC  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    301 GAGAGCAAATAATGATGAAAATAAACTTTCCCTTTGTTTAATTCAGGAAAAATG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAGAGCAAATAATGATGAAAATAAACTTTCCCTTTGTTTAATTCAGGAAAAATG  360

Qy    361 ATGAGGACCAAAATCAATGAATAAGGAAAATGTTTCCAAATTGG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAGGACCAAAATCAATGAATAAGGAAAATGTTTCCAAATTGG  420

Qy    421 TAATTAAGTATTTGTTCCTTGGGAAGACACTTCCATGTGAGCTTGATGGGAAAATGGGAA  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TAATTAAGTATTTGTTCCTTGGGAAGACACTTCCATGTGAGCTTGATGGGAAAATGGGAA  480

Qy    481 AAACGTCAAAAGCATGACATGATCTGATCAGATCCCAAAGTCGATTATTATTTAAAACCAGAT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAACGTCAAAAGCATGACATGATCTGATCAGATCCCAAAGTCGATTATTATTTAAAACCAGAT  540

Qy    541 GGCATCACTCTGGGAGGCAAGTTCAGGAGTTCATGTTAGCAAAGGACATAACAATAAC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGCATCACTCTGGGAGGCAAGTTCAGGAGTTCATGTTAGCAAAGGACATAACAATAAC  600

Qy    601 AGCAAAATCAAAATTCCGCAAATGCGAGGAGGAAATGGGACTGGGAAAAGCTTTCATAAC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCAAAATCAAAATTCCGCAAATGCGAGGAGGAAATGGGACTGGGAAAAGCTTTCATAAC  660

Qy    661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCATACCAGGGAACACAAA  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCGTCTATACCAGGGAACACAAA  720

Qy    721 ATTGACTGGGCTAAGCCTGACTTTCAAGGAGAGCAGCAGATGATGAGAGACTGAGCA  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATTGACTGGGCTAAGCCTGACTTTCAAGGAGAGCAGCAGATGATGAGAGACTGAGCA  780

Qy    781 GACATGTTAAAAGCAACACAGACATTGTGAGCCTTCAAAGCAGCAGTGCCCTCAGCA  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GACATGTTAAAAGCAACACAGACATTGTGAGCCTTCAAAGCAGCAGTGCCCTCAGCA  840

Qy    841 GGGACCCTGAGGCATTGCCTTAGGAAGGCCAGTTTTCTTAAGAAATCTTAAGAAACTC  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGGACCCTGAGGCATTGCCTTAGGAAGGCCAGTTTTCTTAAGAAATCTTAAGAAACTC  900

Qy    901 TTGAAAGATCATGATGAATTTAACCATTTAAGTAATATAAAACAAATGCGATGCATAATCAG  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TTGAAAGATCATGATGAATTTAACCATTTAAGTAATATAAAACAAATGCGATGCATAATCAG  960

Qy    961 TTTAGACATGGGTCCCAATTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTTAGACATGGGTCCCAATTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy   1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTTCAGAATGATC 1080
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Db   1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTTCAGAATGATC 1080

Qy   1081 TGTCATAGCCTCACACACAGGCCCGATGTGTCTGACCTACAACCATCTACAACCCAA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTCATAGCCTCACACACAGGCCCGATGTGTCTGACCTACAACCATCTACAACCCAA 1140

Qy   1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy   1201 TGTGCAGCCCATCCCGCTCCCAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
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Db   1201 TGTGCAGCCCATCCCGCTCCCAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy   1261 TACAGCCAGAAGCTCCGTGAGGGTCTGTGTCTTCAACCTGTATGCTCTAC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TACAGCCAGAAGCTCCGTGAGGGTCTGTGTCTTCAACCTGTATGCTCTAC 1320

Qy   1321 ACCTGACTTGCTCAACCTCTGCCTCCGCACGCCCGCTCAATTTTGTATTGTTAGTAGAGATGGG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ACCTGAGCTTGCTCAACCTCTGCCTCCGCACGCCCGCTAATTTTGTATTGTTAGTAGAGATGGG 1380

Qy   1381 CGGTAGCTGGGACTACAGGCGCCCGGCTAATTTTGTATTTTGTATTGTTAGTAGATTGGG 1440
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Db   1381 CGGTAGCTGGGACTACAGGCGCCCGGCTAATTTTGTATTTTGTATTGTTAGTAGATTGGG 1440

Qy   1441 GTTTCACCATATTAGCCCAGGCTGTCTCGAACTCCTGACCTCAGGTGATCCCACCTC 1500
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Db   1441 GTTTCACCATATTAGCCCAGGCTGTCTTGAACTCCTGACCTCAGGTGATCCCACCTC 1500

Qy   1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTTACAGGGTCAGTGT 1560
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Db   1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTTACAGGGTCAGTGT 1560

Qy   1561 TTAATAAGGAATAACTTGAATGTTTACTAAACACAGGAAACAGACAAAAGCTGTGA 1620
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Db   1561 TTAATAAGGAATAACTTGAATGTTTACTAAACACAGGAAACAGACAAAAGCTGTGA 1620

Qy   1621 TAATTCAGGGATTCTTGGGATGGGAATGGCCATGAGCTGCCTAGTCCCAGAC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TAATTCAGGGATTCTTGGGATGGGAATGGCCATGAGCTGCCTAGTCCCAGAC 1680

Qy   1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy   5221 GCTCCCCAGTATATATAAACCTCTCTGAGCTCGGGCATGAGCCAGCAAGG 5271
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Db   5221 GCTCCCCAGTATATATAAACCTCTCTGAGCTCGGGCATGAGCCAGCAAGG 5271
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Qy   2821  TGGAGTCTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA  2880
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  TGGAGTCTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA  2880

Qy   2881  TGCAAGACGGTCGAAAACCTTGAATCAGGAGACTCGGTTTTCTTCGTTTCTCGTCCATT  2940
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  TGCAAGACGGTCGAAAACCTTGAATCAGGAGACTCGGTTTTCTTCGTTTCTCGTCCATT  2940

Qy   2941  GGTTGGCTGCTGCGACCGTGGCAAGTGTCTTCCTTCCCTGGGCCATAGTCTTCTCTGCT  3000
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  GGTTGGCTGCTGCGACCGTGGCAAGTGTCTTCCTTCCCTGGGCCATAGTCTTCTCTGCT  3000

Qy   3001  ATAAAGACCCTGCAGCTCTCCTGTTCTCGTGTCTCGTGTCTTCCTGTGAACACTTCCCT  3060
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  ATAAAGACCCTGCAGCTCTCCTGTTCTCGTGTCTCGTGTCTTCCTGTGAACACTTCCCT  3060

Qy   3061  GGATGTTGAGAGGGGAGGAGGAGCAGAGCTGAGCGACAGAGCTGAGC...GAGGG  3120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061  GGATGTTGAGAGGGGAGGAGGAGCAGAGCTGAGCGACAGAGCTGAGC...GAGGG  3120

Qy   3121  GGACAGGAAGGCAGGCAGAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC  3180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121  GGACAGGAAGGCAGGCAGAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC  3180

Qy   3181  CAGGACCGAGAGCCACAATGCTCAGGAAAGCTCAATGAACCAACAGCCACATTTTCCT  3240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181  CAGGACCGAGAGCCACAATGCTCAGGAAAGCTCAATGAACCAACAGCCACATTTTCCT  3240

Qy   3241  TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGT  3300
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Db   3241  TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGT  3300

Qy   3301  GGTAGCTTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG  3360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301  GGTAGCTTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTC  3360

Qy   3361  TTAAACTTTTCACCCTGACCAGCAGCTCAGCTGCTGCAGACGCACGG  3420
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   3361  TTAAACTTTTCACCCTGACCAGCAGCTCAGCTGCTGCAGACGCACGG  3420

Qy   3421  AGTGACCTGCAGCAGGGAGAGAAAAGAGAGGGGATAGTGTATGAGCAAGAAAAG  3480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421  AGTGACCTGCAGCAGGGAGAGAAAAGAGAGGGGATAGTGTATGAGCAAGAAAAG  3480

Qy   3481  ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG  3540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481  ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG  3540

Qy   3541  GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAATCAGTTCAAGGGAAGTCGGGAGA  3600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541  GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAATCAGTTCAAGGGAAGTCGGGAGA  3600

Qy   3601  CCTGATTTCTAATACTATATTTTCCTTTACAAGCTGAGTAATTCTGAGTAATTCTGAGCAAG  3660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601  CCTGATTTCTAATACTATATTTTCCTTTACAAGCTGAGTAATTCTGAGTAATTCTGAGCAAG  3660

Qy   3661  GTAGTAACTGAGGCTGTAAGGCTGGGAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT  3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661  GTAGTAACTGAGGCTGTAAGGCTGGGAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT  3720

Qy   3721  GGAGTTAGCAGCACAAGGGCCAATCAAGGGCAATCCCGTTCTTTAACAGGAGAAACATTCCTAAGAG  3780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721  GGAGTTAGCAGCACAAGGGCCAATCAAGGGCAATCCCGTTCTTTAACAGGAGAAACATTCCTAAGAG  3780

Qy   3781  TAAAGCCAAACAGATTCAAGCGACTATATGATTGGTTTTTTGAAAAAT  3840
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   3781  TAAAGCCAAACAGATTCAAGCGACTATATGATTGGTTTTTTGAAAAAT  3840

Qy   3841  CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGACTAGTACCCTTGGTTCAGCTG  3900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841  CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGACTAGTACCCTTTGGTTCAGCTG  3900

Qy   3901  TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAAGTTGTCTTAACTGCAACCAATCAAAA  3960
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Qy   1741  CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG  1800
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Db   1741  CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG  1800

Qy   1801  TTCCATTTGGGGCCATCTGTGTGTGTATAGGGAGGAGGGCATACCCCAGAGACTCCT  1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  TTCCATTTGGGGCCATCTGTGTGTGTATAGGGAGGAGGGCATACCCCAGAGACTCCT  1860

Qy   1861  TGAAGCCCCCGGCAGAGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC  1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  TGAAGCCCCCGGCAGAGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC  1920

Qy   1921  TGGGTGTCCTGAGCAACCTGCAGCCCGTGCCACTGGTGTTTGTTGTTTATCACTCTCTAGG  1980
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  TGGGTGTCCTGAGCAACCTGCAGCCCGTGCCACTGGTGTTTGTTGTTTATCACTCTCTAGG  1980

Qy   1981  GACCTGTTGCTTTCTATTTCTGTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT  2040
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  GACCTGTTGCTTTCTATTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT  2040

Qy   2041  TATTGAGTACTTATATCTGCCAAGACACCAGACAAAATGGTGAGCAAAGCAGTCACTGC  2100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  TATTGAGTACTTATATCTGCCAAGACACCAGACAAAATGGTGAGCAAAGCAGTCACTGC  2100

Qy   2101  CCTACCTTCGTCGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAAATTAATAGCCA  2160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  CCTACCTTCGTCGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAAATTAATAGCCA  2160

Qy   2161  GCCAACTTAAACCCAGTCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTCGC  2220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  GCCAACTTAAACCCAGTCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTCGC  2220

Qy   2221  AGCATCCCTTAACAAGGCCACCTCCCTGCTCCTCCATCCGTGCCCCGAGG  2280
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  AGCATCCCTTAACAAGGCCACCTCCCTGCTCCTCCATCCGTGCCCCGAGG  2280

Qy   2281  CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCATCAGTCACAGCCTGCAGCTGGCCT  2340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCATCAGTCACAGCCTGCAGCTGGCCT  2340

Qy   2341  GCCTCGCTTCCCGTGAATCGTCCGGTGCATCTGGTGCATCTGAGCTGGAGACTCTTGGCTCCAGGCT  2400
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Db   2341  GCCTCGCTTCCCGTGAATCGTCCGGTGCATCTGGTGCATCTGAGCTGGAGACTCTTGGCTCCAGGCT  2400

Qy   2401  CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGGACAGTGTTTC  2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGGACAGTGTTTC  2460

Qy   2461  CTTCAGAGGGGAAAGGGGCCTCCACGTCCACGTCCCACCATCCAGGAGAATTCCAGGAGGATGCAGGGAG  2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  CTTCAGAGGGGAAAGGGGCCTCCACGTCCACGTCCCACCATCCAGGAGAATTCCAGGAGGATGCAGGGAG  2520

Qy   2521  TGGGGACGGGGCTGAGCGGGGCTGGTGCTGAGCGGGGCTGGTGCTGAAAGGGCAGGAAAGGGCAGGAAAGGTTTTCCGTTCCGTTC  2580
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  TGGGGACGGGGCTGAGCGGGGCTGGTGCTGAGCGGGGCTGGTGCTGAAAGGGCAGGAAAGGGCAGGAAAGGTTTTCCGTTCCGTTC  2580

Qy   2581  GCTGCCCAGATGTTCAGTGTTGTTCAGTGTTGTTCACGGGGCTTAATTCCTAGGCCGTTAATTCATGAGGAGAAGTGAC  2640
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  GCTGCCCAGATGTTCAGTGTTGTTCAGTGTTGTTCACGGGGCTTAATTCCTAGGCCGTTAATTCATGAGGAGAAGTGAC  2640

Qy   2641  CTTTTATCTTTTCTCTGCTTCGTTCATTTCGTTCATTTCGTTCATTCATTGAGGGATGCAGTTTC  2700
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  CTTTTATCTTTTCTCTGCTTCGTTCATTTCGTTCATTTCGTTCATTCATTGAGGGATGCAGTTTC  2700

Qy   2701  ATAAAGTCAGCTGTAAAATTCAGGGTGTGCATGGTTTTCCTTCACGGAAGGCCTTTAT  2760
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Db   2701  ATAAAGTCAGCTGTAAAATTCAGGGTGTGCATGGTTTTCCTTCACGGAAGGCCTTTAT  2760

Qy   2761  TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC  2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC  2820
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Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3901 TAAACAAACCCAGTTGTAAATGTCTCAAGTTCAGGCTTCAGCTTCCACATCTGGAGCTTAACTGACAGACCAATCAAAA 3960
Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGCTGAGGTGAGTGAGTTAACAACATAAAGT 4020
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Qy   4021 AGTTTGGAAATATTACTTCACAAGTAATGACACTGTTGTGTATTAACAACATAAAGT 4080
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Qy   4381 TTATACTATTACAGTTGTGTCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440
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Qy   4441 CTTTGAAATTAGACCTCCTGCTGCTAATCTTGTTTTTAACATATTAATAAAACATGTTTTAAA 4500
Db   4441 CTTTGAAATTAGACCTCCTGCTGCTAATCTTGTTTTTAACATATTAATAAAACATGTTTTAAA 4500
Qy   4501 ATTTTGATATTTGATAATCATATTTCATTCATTGTTCCTTGTAATCTATATTT 4560
Db   4501 ATTTTGATATTTGATAATCATATTTCATTCATTGTTCCTTGTAATCTATATTT 4560
Qy   4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCACCAATGAGGTCTTGG 4620
Db   4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCACCAATGAGGTCTTGG 4620
Qy   4621 CATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680
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Qy   4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGTATACACAGTGTGTTTAAAGCTAGGGGTG 4740
Db   4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGTATACACAGTGTGTTTAAAGCTAGGGGTG 4740
Qy   4741 AGGGGGGAAATCTGCCGCTCTATAGGAATGCTCTCCCGAGCCTGGTAGGGTGCTGTC 4800
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Qy   4801 CTTGTGTTCTCGGCTGGCTGTTATTTTCTCGTCCCGTCCTGCTACGTCTTAAAGGACTTGTTT 4860
Db   4801 CTTGTGTTCTCGGCTGGCTGTTATTTTCTCGTCCCGTCCTGCTACGTCTTAAAGGACTTGTTT 4860
Qy   4861 GGAATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTCTCAATGAGTTTGCAGAG 4920
Db   4861 GGAATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTCTCAATGAGTTTGCAGAG 4920
Qy   4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980
Db   4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980
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Db   4981 TGTAAGTGTGTACGTGTGTGTGTGTGTGTATGGGGTATGGGGTGCATAAATTGGAGTGTTCTTT 5040
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Qy   5101 CAAACAGACTTCTGGAAGTTATTTTCTAAGAACTTGCTCGGCAGCGTGAAGGCAACCCC 5160
Db   5101 CAAACAGACTTCTGGAAGTTATTTTCTAAGAACTTGCTCGGCAGCGTGAAGGCAACCCC 5160
Qy   5161 CCTGTGCACAGCCCACCCAGCCACCTCGTCTTCCCCATGAAGGGCTG 5220
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Qy   5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAGGCCAAGG 5271
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RESULT 4
US-08-938-669A-1
; Sequence 1, Application US/08938669A
; Patent No. 6171788
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
; TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
; TITLE OF INVENTION: RELATED DISEASES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,669A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/791,154
; FILING DATE: 28-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mendelson, Elliot
; REGISTRATION NUMBER: P-42,878
; REFERENCE/DOCKET NUMBER: 07425-0034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 383-6857
; TELEFAX: 202 383-6610
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5300 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-938-669A-1

Query Match   99.5%;   Score 5246.4;   DB 3;   Length 5300;
Best Local Similarity 99.9%;   Pred. No. 0;
Matches 5269;   Conservative 0;   Mismatches 1;   Indels 2;   Gaps 2;

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Qy      1 ATCTTTGTTCAGTTTACCTCAGGCTATTATGGGCTATTATGAATGAAATGAGATAACCAATGTGAAAG 60
Db      1 ATCTTTGTTCAGTTTACCTCAGGCTATTATGAATGAAATGAGATAACCAATGTGAAAG 60
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Qy    61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA  120
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Db    61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA  120

Qy   121  GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCGTGTCTGCTCTTATTTTAGTGA  180
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Db   121  GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCGTGTCTGCTCTTATTTTAGTGA  180

Qy   181  CAGATGTTGCTCCTGACAGAGAGCTATTCTTCAGGAAACATCACATCCAATATGTAAATC  240
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Db   181  CAGATGTTGCTCCTGACAGAGAGCTATTCTTCAGGAAACATCACATCCAATATGTAAATC  240

Qy   241  CATCAAACAGGAGCTAAGAAACAGAGATGGGCACTTGCCCAAGGAAAAATGCCAG  300
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Db   241  CATCAAACAGGAGCTAAGAAACAGAGATGGGCACTTGCCCAAGGAAAAATGCCAG  300

Qy   301  GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTGTTTTAATTTCAGGAAAAATGG  360
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Db   361  GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTGTTTTAATTTCAGGAAAAAATG  360

Qy   361  ATGAGGACCAAAATCAATGAATAAGGAAAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG  420
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Db   361  ATGAGGACCAAAATCAATGAATAAGGAAAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG  420

Qy   421  TAATTAAGTATTTGTTCCTTGGGAAGAGACCTGAGCTGAGTGAAATGGGAA  480
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Db   421  TAATTAAGTATTTGTTCCTTGGGAAGAGACCTGAGCTGAGTGAAATGGGAA  480

Qy   481  AAACGTCAAAAGCATGATCAGATCAGATGGATTATTATTTTAAAAACCAGAT  540
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Db   481  AAACGTCAAAAGCATGATCAGATCAGATGGATTATTATTTTAAAAACCAGAT  540

Qy   541  GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGACATAACAATAAC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGACATAACAATAAC  600

Qy   601  AGCAAAATCAAAATCCGCAAATGGGACTGGGAAAATGGGACTCTTTCATAAC  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  AGCAAAATCAAAATCCGCAAATGGGACTGGGAAAATGGGACTCTTTCATAAC  660

Qy   661  AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCAACACCTCCCAAGGGAACACAAAA  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCAACACCTCCCAAGGGAACACAAAA  720

Qy   721  ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAGAGCAAAGACAAAA  780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAGAGCAAAGACAAAA  780

Qy   781  GACATGGTTAAAAGGCAACCAGAACATTGTAGCCTCAAAGCAGTGCCCCTCAGCA  840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GACATGGTTAAAAGGCAACCAGAACATTGTAGCCTCAAAGCAGTGCCCCTCAGCA  840

Qy   841  GGGACCCTGAGGCATTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  GGGACCCTGAGGCATTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC  900

Qy   901  TTGAAAGATCATGAATTTAACCATTTAAGTATAAAACAAATATGCGATGCATAAATCAG  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  TTGAAAGATCATGAATTTAACCATTTAAGTATAAAACAAATATGCGATGCATAAATCAG  960

Qy   961  TTTAGACATGGGTCCCAATTTATATAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  TTTAGACATGGGTCCCAATTTATATAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020

Qy  1021  GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTTCAGAATGATC  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTTCAGAATGATC  1080

Qy  1081  TGTCATAGCCTCACACACAGGCCCGATGTGTTCTGACCTACAACCACATCTACAACCCA  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  TGTCATAGCCCTCACACACAGGCCCGATGTGTTCTGACCTACAACCACATCTACAACCCA  1140


Qy  1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGTCCCATTACAAATGCCACCTCCCC  1200
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Db  1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGTCCCATTACAAATGCCACCTCCCC  1200

Qy  1201  TGTGAGCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTCAACCTCTGTATGCTCTAC  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  TGTGAGCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTCAACCTCTGTATGCTCTAC  1260

Qy  1261  TACAGGCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTCAACCTCTGTATGCTCTAC  1320
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Db  1261  TACAGGCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTCAACCTCTGTATGCTCTAC  1320

Qy  1321  ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCGTGTCTCAGCCTCC  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCGTGTCTCAGCCTCC  1380

Qy  1381  CGGTAGCTGGGACTACAGGCGCACGGCGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG  1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CGGTAGCTGGGACTACAGGCGCACGGCGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG  1440

Qy  1441  GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC  1500

Qy  1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCCGCCAAGGGTCAGTGT  1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCCGCCAAGGGTCAGTGT  1560

Qy  1561  TTAATAAGGAATAACTTGAATGGTTACTAAACAGAGGAACAGGAAACAGAAAGCTGTGA  1620
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Db  1561  TTAATAAGGAATAACTTGAATGGTTACTAAACAGAGGAACAGGAAACAGAAAGCTGTGA  1620

Qy  1621  TAATTTCAGGGATGGGGAATGCTCCATCTCATTTTCAGGCTAAGCTAAGTGCCTCCCAGAC  1680
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Db  1621  TAATTTCAGGGATGGGGAATGCTCCATCTCATTTTCAGGCTAAGCTAAGTGCCTCCCAGAC  1680

Qy  1681  CACCATGTCTCCATCACTTCTTCCCTCCACATTTTCAGGCTAAGTTACCATTTTATT  1740
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Db  1681  CACCATGTCTCCATCACTTCTTCCCTCCACATTTTCAGGCTAAGTTACCATTTTATT  1740

Qy  1741  CACTGTCTTTGTGGGGCCATCTGTGTGTGTGTATAGGGGAGGGGCATACCCCGAGACTCCT  1800
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Db  1741  CACCATGTTTGTGGGGCCATCTGTGTGTGTGTATAGGGGAGGGGCATACCCCGAGACTCCT  1800

Qy  1801  TTCCATTTGGGCCAGAGGTTTCCTCTCCAGCTGGGGGAGCACCCGGGGTCC  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  TTCCATTTGGGCCAGAGGTTTCCTCTCCAGCTGGGGGAGCACCCGGGGTCC  1860

Qy  1861  TGAAGCCCCGGCAGAGGTTCCTGCCAGTTGTCAAGCAGCAGTGCCCTGCAGGAGACTCCT  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  TGAAGCCCCGGCAGAGGTTCCTGCCAGTTGTCAAGCAGCAGTGCCCTGCAGGAGACTCCT  1920

Qy  1921  TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTCGGTGTTTGTTTGTTATCACTCTCTAGG  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTCGGTGTTTGTTTGTTATCACTCTCTAGG  1980

Qy  1981  GACCTGTTGCTTTTCTATTTCGTTGACTGTTCATTCATCCAGGCATTCATTGACAATT  2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  GACCTGTTGCTTTTCTATTTCGTTGACTGTTCATTCATCCAGGCATTCATTGACAATT  2040

Qy  2041  TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC  2100
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Db  2041  TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC  2100

Qy  2101  CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAGAGAAATTAATAGCCA  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAGAGAAATTAATAGCCA  2160

Qy  2161  GCCAACTTAAACCCAGTGCTGCTAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC  2220
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Db  2161  GCCAACTTAAACCCAGTGCTGCTAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC  2220

Qy  2221  AGCATCCCTTAACAGGCCACCTCCTAGCGCCCCTGCTCCTCATCGTGCCCGGAGG  2280
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Qy  3361  TTAAACTTTTCACCCTGACCAGCAGCACCCCAGCAGCTCAGCAGTGACTGCTGACAGCACGG  3420
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Db  3361  TTAAACTTTTCACCCTGACCAGCAGCACCCCAGCAGCTCAGCAGTGACTGCTGACAGCACGG  3420

Qy  3421  AGTGACCTGCAGCGCAGGGGAGGAGAAGAGAGGATAGTGTATGAGCAAGAAAG  3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421  AGTGACCTGCAGCGCAGGGGAGGAGAAGAGAGGATAGTGTATGAGCAAGAAAG  3480

Qy  3481  ACAGATTCATTCAAGGGCAGTGGGAATTGACCACCAGGGATTATAGTCCACGTGATCCTGG  3540
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Db  3481  ACAGATTCATTCAAGGGCAGTGGGAATTGACCACCAGGGATTATAGTCCACGTGATCCTGG  3540

Qy  3541  GTTCTAGGAGGCAGGGCTATATTGTGGGGGAAAAAATCAGTCAAGGGAGTCGGGAGA  3600
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Db  3541  GTTCTAGGAGGCAGGGCTATATTGTGGGGGAAAAAATCAGTCAAGGGAGTCGGGAGA  3600

Qy  3601  CCTGATTTCTAATACTATATTTTCCTTACAAGCTGAGTAATTCTGAGCAAGTCACCAAG  3660
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Db  3601  CCTGATTTCTAATACTATATTTTCCTTACAAGCTGAGTAATTCTGAGCAAGTCACCAAG  3660

Qy  3661  GTAGTAACTGAGGCTGTGTAAGATTACTTAGTTTCTCCCTTATTAGGAACTCTTTTTCTCTGT  3720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661  GTAGTAACTGAGGCTGTGTAAGATTACTTAGTTTCTCCCTTATTAGGAACTCTTTTTCTCTGT  3720

Qy  3721  GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAGAG  3780
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Db  3721  GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAGAG  3780

Qy  3781  TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT  3840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781  TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT  3840

Qy  3841  CATTTCAGCCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTAGCCCTTTGGTACCCTG  3900
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Db  3841  CATTTCAGCCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTAGCCCTTTGGTACCCTG  3900

Qy  3901  TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGCCTTAACTGCGAACCAATCAAA-  3959
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Db  3901  TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGCCTTAACTGCGAACCAATCAAAT  3960

Qy  3960  AAGAATAGAATCTTTAGAGCAAACTGTGTTCTCCCACATCTGGAGGTGAGTCTGCCAGGG  4019
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Db  3961  AAGAATAGAATCTTTAGAGCAAACTGTGTTCTCCCAC-TCTGGAGGTGAGTCTGCCAGGG  4019

Qy  4020  CAGTTTGGAAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG  4079
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Db  4020  CAGTTTGGAAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG  4079

Qy  4080  TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTTTCTCTTTTGGTTTATTAAGCA  4139
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Db  4080  TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTTTCTCTTTTGGTTTATTAAGCA  4139

Qy  4140  TTTATTGGCTATTGCCATTTGCTTTTGTTTTTCTTTTGGTTTATTAACAGTTTGTCATTACCAATAGAGCA  4199
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Db  4140  TTTATTGGCTATTGCCATTTGCTTTTGTTTTTCTTTTGGTTTATTAATGTAAAGCA  4199

Qy  4200  GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT  4259
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Db  4200  GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT  4259

Qy  4260  TTGTTTTTACCACCTTCTAACTAAAGAGCCATAA  4319
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Db  4260  TTGTTTTTACCACCTTCTAACTAAATTTTATTCCATTGCGAATAGAGCCATAA  4319

Qy  4320  ACTCAAAGTGGTAATAACAGTACCTGATTTTGTCATTACCAATAGAATCACAGACAT  4379
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Db  4320  ACTCAAAGTGGTAATAACAGTACCTGATTTTGTCATTACCAATAGAATCACAGACAT  4379

Qy  4380  TTTATACTATATTACAGTTGTTGCAGATACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT  4439
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4380  TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT  4439
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Db  2221  AGCATCCCTTAACAAGGCCACCTCCCTAGGCGCCCCTGCTCCTCCATCGTGCCCCGGAGG  2280

Qy  2281  CCCCCAAGCCGAGTCTTCCAAGCCTCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT  2340
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Db  2281  CCCCCAAGCCGAGTCTTCCAAGCCTCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT  2340

Qy  2341  GCCTCGCTTCCCGTGAATCGTCTCGTGCATCGGAGACTCCTTGGCTCCAGGCT  2400
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Db  2341  GCCTCGCTTCCCGTGAATCGTCTCGTGCATCGGAGACTCCTTGGCTCCAGGCT  2400

Qy  2401  CCAGAAAGGAAATGAGAGAGGAAACTAGTCTAACGAGAATCTCGAGGGGACAGTGTTTC  2460
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Db  2401  CCAGAAAGGAAATGAGAGAGGAAACTAGTCTAACGAGAATCTCGAGGGGACAGTGTTTC  2460

Qy  2461  CTCAGAGGGAAAGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG  2520
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Db  2461  CTCAGAGGGAAAGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG  2520

Qy  2521  TGGGGACCGCTGGGGCTGAGCGGTGCTGAGGAGAGGTGAAAAGGGCAAGGCTGAA  2580
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Db  2521  TGGGGACCGCTGGGGCTGAGCGGTGCTGAGGAGAGGTGAAAAGGGCAAGGCTGAA  2580

Qy  2581  GCTGCCCAGATGTTCAGTGTTGTTCACGGGGGTCTGGAGTTTTCCGTTCCTGTGAGC  2640
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Db  2581  GCTGCCCAGATGTTCAGTGTTGTTCACGGGGGTCTGGAGTTTTCCGTTCCTGTGAGC  2640

Qy  2641  CTTTTTATCTTTTCTCTGCTTGGAGGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC  2700
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Db  2641  CTTTTTATCTTTTCTCTGCTTGGAGGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC  2700

Qy  2701  ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTCCTTCACGGCCTTTAT  2760
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Db  2701  ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTCCTTCACGGCCTTTAT  2760

Qy  2761  TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACCGGAAGAAGTGAC  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACCGGAAGAAGTGAC  2820

Qy  2821  TGGAGTCTTTTCATGTCTTCTCTGGGCAACTACTCAGCCCTGTGGTTGGACTTGGCTTA  2880
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Db  2821  TGGAGTCTTTTCATGTCTTCTCTGGGCAACTACTCAGCCCTGTGGTTGGACTTGGCTTA  2880

Qy  2881  TGCAAGACGGTCGAAAACCTTGGAATCAGGAGAACTCGGTTTTTCTTCTTCTGGTTCTGCCATT  2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  TGCAAGACGGTCGAAAACCTTGGAATCAGGAGAACTCGGTTTTTCTTCTTCTGGTTCTGCCATT  2940

Qy  2941  GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCGGGCCATAGTCTTCTTCTGCT  3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCGGGCCATAGTCTTCTTCTGCT  3000

Qy  3001  ATAAAGACCCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCGTGATTCTCTGTGAGGGG  3060
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Db  3001  ATAAAGACCCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCGTGATTCTCTGTGAGGGG  3060

Qy  3061  GGATGTTGAGAGGGGAAGGAGCCCAGAGCCACAGGGGAGTGGAGGG  3120
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Qy  3121  GGACAGGAAGGCAGGGCAGGCAGAGCTGGGTCGTGCTTCCATCGATCAGTGCTCAGACTC  3180
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Db  3121  GGACAGGAAGGCAGGGCAGGCAGAGCTGGGTCGTGCTTCCATCGATCAGTGCTCAGACTC  3180

Qy  3181  CAGGACCGAGAGCCGAGAGCCAGGCCACAATGCTTCAGGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT  3240
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Db  3181  CAGGACCGAGAGCCGAGAGCCAGGCCACAATGCTTCAGGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT  3240

Qy  3241  TCCCTAAGCACATAGACAATGGCATTTGCCAATAACCAAAAGAGATTGCAGAGACTAACTGGT  3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  TCCCTAAGCACATAGACAATGGCATTTGCCAATAACCAAAAGAGATTGCAGAGACTAACTGGT  3300

Qy  3301  GGTTAGCTTTTGCCTTGGCATTCAAAAACTGGGCCAGAGCAGCAAGTGGAAATGCCAGAGATTG  3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301  GGTTAGCTTTTGCCTTGGCATTCAAAAACTGGGCCAGAGCAGCAAGTGGAAATGCCAGAGATTG  3360
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; SEQ ID NO 1
; LENGTH: 5300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-1

Query Match       99.5%;    Score 5246.4;    DB 3;    Length 5300;
Best Local Similarity  99.9%;    Pred. No. 0;
Matches 5269;    Conservative  0;    Mismatches  1;    Indels  2;    Gaps  2;

Qy    1   ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1   ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG   60

Qy   61   TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGATGATAAAGAAGATCA  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61   TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGATGATAAAGAAGATCA  120

Qy  121   GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAAGTGTCTGCTCTTATTTAGTGA     180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121   GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAAGTGTCTGCTCTTATTTAGTGA     180

Qy  181   CAGATGTTGCTCCTGACGAGAGCTATTCTTCAGGAAACATCATCCAATATGTAAATC     240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181   CAGATGTTGCTCCTGACGAGAGCTATTCTTCAGGAAACATCACCAATATGTAAATC      240

Qy  241   CATCAAACAGGAGCTAAGAAACAGGAATGAGATGACCACTTGCCCAAGGAAAATGGCCAG   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241   CATCAAACAGGAGCTAAGAAACAGGAATGAGATGACCACTTGCCCAAGGAAAATGGCCAG   300

Qy  301   GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTGTTTTAATTTCAGGAAAAATG   360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301   GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTGTTTTAATTTCAGGAAAAATG   360

Qy  361   ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAGATGTTTCCAAATTGG   420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361   ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAGATGTTTCCAAATTGG   420

Qy  421   TAATTAAGTATTTGTTCCTTGGGAAGACACCTCCATGTGAGCTTGATGGGAAATGGGAA   480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421   TAATTAAGTATTTGTTCCTTGGGAAGACACCTCCATGTGAGCTTGATGGGAAATGGGAA   480

Qy  481   AAACGTCAAAGCATGATCTGATCAGATCGATCAGATGATTATTTTAAAACCAGAT     540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481   AAACGTCAAAGCATGATCTGATCAGATCGATCAGATGATTATTTTAAAACCAGAT     540

Qy  541   GGCATCACTCTGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAGGACATAACAATAAC   600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541   GGCATCACTCTGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAGGACATAACAATAAC   600

Qy  601   AGCAAAATCAAAATTCCGCAAATTCCGCAAATGGGGACTCGGGAAAGCTTTCATAAC     660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601   AGCAAAATCAAAATTCCGCAAATTCCGCAAATGGGGACTCGGGAAAGCTTTCATAAC     660

Qy  661   AGTGATTAGGCAGTTGACCATGTTCGCAACACTTGCCAACACCTCTATACCAGGAACAAAA  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661   AGTGATTAGGCAGTTGACCATGTTCGCAACACTTGCCAACACCTCTATACCAGGAACAAAA  720

Qy  721   ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAtATGAAAACTGAGAGCAAAACAAAA   780
          |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db  721   ATTGACTGGGCTAAGCCTGGACTTTCAAGGGGAAATGAAAACTGAGAGCAAAACAAAA   780

Qy  781   GACATGGTTAAAAGGCAACCACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781   GACATGGTTAAAAGGCAACCACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA  840

Qy  841   GGGACCCCTGAGGCCAGTTTGCCTTAGGAAGGCCAGTTTTTCTTAAGGAATCTTAAGAAACTC  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841   GGGACCCCTGAGGCCAGTTTGCCTTAGGAAGGCCAGTTTTTCTTAAGGAATCTTAAGAAACTC  900

Qy  901   TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAAATATGCGATGCATAATAATCAG  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901   TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAAATATGCGATGCATAATAATCAG  960
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Qy  4440   ACTTTGAAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAACATGTTTAA   4499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4440   ACTTTGAAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAACATGTTTAA   4499

Qy  4500   AATTTTGATATTTGATAATCATATTCATTATCATTGTTCCTTTGTAATCTATATATT      4559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4500   AATTTTGATATTTGATAATCATATTCATTATCATTGTTCCTTTGTAATCTATATATT      4559

Qy  4560   TATATATTTGAAAAACATCTTTCTGAGAAGAGTTCCCAGATTTCACCCAATGAGGTTCTTG   4619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4560   TATATATTTGAAAAACATCTTTCTGAGAAGAGTTCCCAGATTTCACCCAATGAGGTTCTTG   4619

Qy  4620   GCATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTCGTGCCTGAG   4679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4620   GCATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTCGTGCCTGAG   4679

Qy  4680   ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTGTGTTTAAAGCTAGGGGT   4739
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4680   ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTGTGTTTAAAGCTAGGGGT   4739

Qy  4740   GAGGGGGAAATCTGCCGCTTCTATAGGAAATGCTCTCCCTGAGCCTGGTAGGGTGCTGT   4799
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4740   GAGGGGGAAATCTGCCGCTTCTATAGGAAATGCTCTCCCTGAGCCTGGTAGGGTGCTGT   4799

Qy  4800   CCTTGTGTTCTGGCTGTGTTATTTTCTCTGTCCCTGCTACGTCTAAAGGACTTGTT      4859
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4800   CCTTGTGTTCTGGCTGTGTTATTTTCTCTGTCCCTGCTACGTCTAAAGGACTTGTT      4859

Qy  4860   TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGTTCTCAATGAGTTTGCAGA   4919
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4860   TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGTTCTCAATGAGTTTGCAGA   4919

Qy  4920   GTGAATGGAAAATATAAACTAGAAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG   4979
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4920   GTGAATGGAAAATATAAACTAGAAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG   4979

Qy  4980   GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT    5039
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4980   GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT    5039

Qy  5040   ATAGGAACTATTATTGGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT   5099
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5040   ATAGGAACTATTATTGGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT   5099

Qy  5100   CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC   5159
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5100   CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC   5159

Qy  5160   CCCTGTGTGCACAGCCCCACCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT   5219
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5160   CCCTGTGTGCACAGCCCCACCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT   5219

Qy  5220   GGCTCCCCAGTATATAAACCTCTCTGGAGCTCGGCATGAGCCGGCCAGCAAGG      5271
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5220   GGCTCCCCAGTATATAAACCTCTCTGGAGCTCGGCATGAGCCGGCCAGCAAGG      5271
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Qy  2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGTGAGCAAAGCAGTCACTGC 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGTGAGCAAAGCAGTCACTGC 2100

Qy  2101 CCTACCTTCGTGGAGTGACAGTTTCTCATGGAAGACGTGCAGAAGACGTGCAGAAATTAATAGGCA 2160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 CCTACCTTCGTGGAGTGACAGTTTCTCATGGAAGACGTGCAGAAGACGTGCAGAAATTAATAGGCCA 2160

Qy  2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy  2221 AGCATCCCTAACAAGGCCACCTCCCTAGGCCCCCTGCCTCCATCGTGCCCCGGAGG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 AGCATCCCTAACAAGGCCACCTCCCTAGGCCCCCTGCCTCCATCGTGCCCCGGAGG 2280

Qy  2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGGCGTGCAGCTGGCCT 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGGCGTGCAGCTGGCCT 2340

Qy  2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy  2401 CCAGAAAGGAAATGAGAGGGAAACTAGTCAACGGAGAATCTGAGGAGGTCGGGGACAGTGTTTC 2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 CCAGAAAGGAAATGAGAGGGAAACTAGTCAACGGAGAATCTGAGGAGGTCGGGGACAGTGTTTC 2460

Qy  2461 CTCAGAGGGAAAGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CTCAGAGGGAAAGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520

Qy  2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAGACGTGAAAGGCAAGGCTGAA 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAGACGTGAAAGGCAAGGCTGAA 2580

Qy  2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTCCTGCTTCCTGTGAGC 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTCCTGCTTCCTGTGAGC 2640

Qy  2641 CTTTTTATCTTTCTCTGCTTGGAGAGGAAGAGTCTATTTCATGAAGGATGCAGTTTC 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 CTTTTTATCTTTCTCTGCTTGGAGAGGAAGAGTCTATTTCATGAAGGATGCAGTTTC 2700

Qy  2701 ATAAAGTCAGCTGTTAAAATTCAGGGGTGCATGGGTTTCCTTCACGAAGGCCTTTAT 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 ATAAAGTCAGCTGTTAAAATTCAGGGGTGCATGGGTTTCCTTCACGAAGGCCTTTAT 2760

Qy  2761 TTAATGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTAATTCACGGAAGAGTGAC 2820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 TTAATGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTAATTCACGGAAGAGTGAC 2820

Qy  2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGACTTGGCTTA 2880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGACTTGGCTTA 2880

Qy  2881 TGCAAGACGGTGAAAACCTTGAATCAGGAGGGCATACCCCAGAGACTCCT 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 TGCAAGACGGTGAAAACCTTGAATCAGGAGGGCATACCCCAGAGACTCCATT 2940

Qy  2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTTCTCCTTCCCGTAATTCACGGAAGAGTGCT 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTTCTCCTTCCCGTAATTCACGGAAGAGTGCT 3000

Qy  3001 ATAAAGACCCTTGCAAGCTCGTGTTCTGTGAACACTTCCCTGATTCTGTGAGGGG 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 ATAAAGACCCTTGCAAGCTCGTGTTCTGTGAACACTTCCCTGATTCTGTGAGGGG 3060

Qy  3061 GGATGTTGAGAGGGGAAGGAGGCAGGAGGGCAGAGCTGAGCAGCTGGAGTTGGAGGG 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 GGATGTTGAGAGGGGAAGGAGGCAGGAGGGCAGAGCTGAGCAGCTGGAGTTGGAGGG 3120

Qy  3121 GGACAGGAGGCAGGCAGAAGCTGGGTGCTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 GGACAGGAGGCAGGCAGAAGCTGGGTGCTGCTCCATCAGTCCTCACTGATCACGTCAGACTC
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Qy   961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy  1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTTCAGAATGATC 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTTCAGAATGATC 1080

Qy  1081 TGTCATAGCCTCCACACACAGGCCCGATGTGTCTGACTACAACCACATCTACAACCCAA 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 TGTCATAGCCTCCACACACAGGCCCGATGTGTCTGACTACAACCACATCTACAACCCAA 1140

Qy  1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCATTACAAATGCCACCTCCCC 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCATTACAAATGCCACCTCCCC 1200

Qy  1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCACTCTAGACTTCTGCATCACGATGT 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy  1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTTCTTACACCTGTATGCTCTAC 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTTCTTACACCTGTATGCTCTAC 1320

Qy  1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy  1381 CGGGTAGCTGGGACTACAGGCGCACGCGCCACCACGCCCGGTAATTTTGTATTGTTAGTAGAGATGGG 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CGGGTAGCTGGGACTACAGGCGCACGCGCCACCACGCCCGGTAATTTTGTATTGTTAGTAGAGATGGG 1440

Qy  1441 GTTTCACCATTATTAGCCCGGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCAGCTC 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 GTTTCACCATTATTAGCCCGGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCAGCTC 1500

Qy  1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGCCATGCACCGCGCCCGGCCAAGGGTCAGTGT 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGCCATGCACCGCGCCCGGCCAAGGGTCAGTGT 1560

Qy  1561 TTAATAAGGAATAACTTGAATGGTTTACTAAAACCAACAGGGAAACAGAGCAAAAGCTGTGA 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 TTAATAAGGAATAACTTGAATGGTTTACTAAAACCAACAGGGAAACAGAGCAAAAGCTGTGA 1620

Qy  1621 TAATTTCAGGGATTCTTGGAATGGGGAATGTGCCATGAAGGGGAGGGGCATACCCGTAGTCCCAGAC 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 TAATTTCAGGGATTCTTGGAATGGGGAATGTGCCATGAAGGGGAGGGGCATACCCGTAGTCCCAGAC 1680

Qy  1681 CACTGGTCCTCATCACACTTTCTTCCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 CACTGGTCCTCATCACACTTTCTTCCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy  1741 CACCATGCTTTGTGTGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 CACCATGCTTTGTGTGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy  1801 TTCCATTTGGGGCCATCTGTGTGTATAGGGTGTGTATAGGGGAGGGGCACTGGTTGTTTATTTT 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 TTCCATTTGGGGCCATCTGTGTGTATAGGGTGTGTATAGGGGAGGGGCACTGGTTGTTTATTTT 1860

Qy  1861 TGAAGCCCCGGCAGAGGTTCCTCTGGGGAGCCCTGCCAAGGGGCATACCCGCAAGCACCCGGGGTCC 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 TGAAGCCCCGGCAGAGGTTCCTCTGGGGAGCCCTGCCAAGGGGCATACCCGCAAGCACCCGGGGTCC 1920

Qy  1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTGTTATCACTTCCTCAGG 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTGTTATCACTTCCTCAGG 1980

Qy  1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
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Qy

Db

Db	GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAATTACATTT	4259
Qy	GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAATTACATTT	4259

RESULT 6
US-08-938-669A-2

```
; Sequence 2, Application US/08938669A
; Patent No. 6171788
; GENERAL INFORMATION:
;   APPLICANT: Nguyen, Thai D.
;   APPLICANT: Polansky, Jon R.
;   TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
;   TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
;   TITLE OF INVENTION: RELATED DISEASES
;   NUMBER OF SEQUENCES: 32
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Howrey & Simon
;     STREET: 1299 Pennsylvania Avenue, N.W.
;     CITY: Washington
;     STATE: DC
;     COUNTRY: USA
;     ZIP: 20004-2402
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/938,669A
;     FILING DATE:
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/791,154
;     FILING DATE: 28-JAN-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Mendelson, Elliot
;     REGISTRATION NUMBER: P-42,878
;   REFERENCE/DOCKET NUMBER: 07425-0034
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 202 383-6857
;     TELEFAX: 202 383-6610
;     TELEX:
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 5304 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
US-08-938-669A-2

Query Match             99.1%;    Score 5224.4;   DB 3;   Length 5304;
Best Local Similarity   99.8%;    Pred. NO. 0;
Matches 5264;   Conservative    0;   Mismatches   6;   Indels   6;   Gaps   3;

Qy         1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAAATGAAATGAGAATAACCAATGTGAAAG   60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAAATGAGAATAACCAATGTGAAAG   60

Qy        61 TCCTATAAACTGTATAGCCTCAGGGATGTATGTCTTTGGCAGGATGATAAAGAATCA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 TCCTATAAACTGTATAGCCTCAGGGATGTATGTCTTTGGCAGGATGATAAAGAATCA  120

Qy       121 GGAAGAAGGAGTATCCACGTTAGCCACGTTAGCCAAGTGTCCAGGCTGTGTCTCTTATTTTAGTGA  180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GGAAGAAGGAGTATCCACGTTAGCCACGTTAGCCAAGTGTCCAGGCTGTGTCTCTTATTTTAGTGA  180

Qy       181 CAGATGTTGCTCCTGACAGAGAAGCTATTCTTCAGGAAAACATCACATCCAATATGGTAAATC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CAGATGTTGCTCCTGACAGAGAAGCTATTCTTCAGGAAAACATCACATCCAATATGGTAAATC  240

Qy       241 CATCAAACAGGAGCTAAGAAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAATGCCAG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CATCAAACAGGAGCTAAGAAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAATGCCAG  300

Qy       301 GAGAGCAAATAATGATGAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GAGAGCAAATAATGATGAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG  360

Qy       361 ATGAGGACCAAAATCAATGAATAAGGAAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 ATGAGGACCAAAATCAATGAATAAGGAAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG  420

Qy       421 TAATTAAGTATTTGTTCCTTGGGAGAGAGAGACCTCCATGTGAGCTTGATGGGAAATGGGAA  480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 TAATTAAGTATTTGTTCCTTGGGAGAGAGAGACCTCCATGTGAGCTTGATGGGAAATGGGAA  480

Qy       481 AAACGTCAAAAGCATGATCATCTGATCAGATCCCAAAGTGGATTATTATTTAAAAACCAGAT  540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 AAACGTCAAAAGCATGATCATCTGATCAGATCCCAAAGTGGATTATTATTTAAAAACCAGAT  540

Qy       541 GGCATCACTCTGGGGAGGCAAGTCATGTTAGCAAAGGACATAACAATAAC  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GGCATCACTCTGGGGAGGCAAGTCATGTTAGCAAAGGACATAACAATAAC  600

Qy       601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGACTGGGAAAGCTTTCATAAC  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGACTGGGAAAGCTTTCATAAC  660

Qy       661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCGTCTATACCAGGGAACACAAAA  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCGTCTATACCAGGGAACACAAAA  720

Qy       721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA  780
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA  780

Qy       781 GACATGGTAAAAGGCAACCAGACAACATTGTGAGCTTCAAAGCAGCAGTGCCCCTCAGCA  840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 GACATGGTAAAAGGCAACCAGACAACATTGTGAGCTTCAAAGCAGCAGTGCCCCTCAGCA  840

Qy       841 GGGACCCTGAGGCATTGCCTTTAGGAAGCCAGTTTCTTAAGGAAATCTTAAGAAACTC  900
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 GGGACCCTGAGGCATTGCCTTTAGGAAGCCAGTTTCTTAAGGAAATCTTAAGAAACTC  900

Qy       901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAAATATGCGATGCATAATCAG  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAAATATGCGATGCATAATCAG  960

Qy       961 TTTAGACATGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 TTTAGACATGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020

Qy      1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTTCAGAATGATC  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTTCAGAATGATC  1080

Qy      1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCATCTACAACCCAA  1140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCATCTACAACCCAA  1140

Qy      1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC  1200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC  1200

Qy      1201 TGTGCAGCCCATCCCGCTCCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 TGTGCAGCCCATCCCGCTCCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT  1260

Qy      1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTCTTCTACACCTACCAATGTGCTCTAC  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTCTTCTACACCTACCAATGTGCTCTAC  1320

Qy      1321 ACCTGAGCTCACTGCAACCTCTGCCTCCTCCCAGTTCAAGCAATTCTCCTGTGTCTCAGCCTC  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 ACCTGAGCTCACTGCAACCTCTGCCTCCTCCCAGTTCAAGCAATTCTCCTGTGTCTCAGCCTC  1380

Qy      1381 CGCGTAGCTGGGACTACAGGCGCACGCCACCGGCCTAATTTTGTATTGTTAGTAGAGATGGG  1440
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 CGCGTAGCTGGGACTACAGGCGCACGCCACCGGCCTAATTTTGTATTGTTAGTAGAGATGGG  1440

Qy      1441 GTTTCACCATATTAGCCCGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCG  1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  1441  GTTTCACCATTATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGTGATCACCCACCTC  1500

Qy  1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCCGCCCGGCCAAGGGTCAGTGT  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCCGCCCGGCCAAGGGTCAGTGT  1560

Qy  1561  TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGAGAAACAGACAAAAAGCTGTGA  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGAGAAACAGACAAAAAGCTGTGA  1620

Qy  1621  TAATTTCAGGGATTCTTGGGATGGGAATGGTGCCATGAGCTGCCTAGTCCCAGAC  1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  TAATTTCAGGGATTCTTGGGATGGGAATGGTGCCATGAGCTGCCTAGTCCCAGAC  1680

Qy  1681  CACTGTGTCCTCATCACTTCTTCCTCATTTCAGGCTAAGTTACCATTTTATT  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  CACTGTGTCCTCATCACTTCTTCCTCATTTCAGGCTAAGTTACCATTTTATT  1740

Qy  1741  CACCATGCTTTTGTGTGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  CACCATGCTTTTGTGTGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG  1800

Qy  1801  TTCCATTTGGGGCCATCTGTGTGTGTATAGGGGAGGAGGCATACCCCAGAGACTCCT  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  TTCCATTTGGGGCCATCTGTGTGTGTATAGGGGAGGAGGCATACCCCAGAGACTCCT  1860

Qy  1861  TGAAGCCCCCGCAGAGGTTTCCTCTCCAGCTGGGGAGCCCTGCAAGCACCCGGGGTCC  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  TGAAGCCCCCGCAGAGGTTTCCTCTCCAGCTGGGGAGCCCTGCAAGCACCCGGGGTCC  1920

Qy  1921  TGGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTCGGTTGTTTGTTATCACTCTCTAGG  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  TGGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTCGGTTGTTTGTTATCACTCTCTAGG  1980

Qy  1981  GACCTGTTGCTTTCTATTTCGTGTGACTCGTTCATTCATTCAGGCATTCATTGACACTAATGTGACAATT  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  GACCTGTTGCTTTCTATTTCGTGTGACTCGTTCATTCATTCAGGCATTCATTGACACTAATGTGACAATT  2040

Qy  2041  TATTGAGTACTTATATCTGCCAGACACCACCAGAGAAATGTGAGCAAAGCAGTCACTGC  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  TATTGAGTACTTATATCTGCCAGACACCACCAGAGAAATGTGAGCAAAGCAGTCACTGC  2100

Qy  2101  CCTACCTTCGTTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAATTAATAGTCA  2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCTACCTTCGTTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAATTAATAGTCA  2160

Qy  2161  GCCAACTTAAACCCAGTGCTGCTGCACCTCCCTAGCGCCTCCTCCCTGCGCGCCCCCGAGG  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GCCAACTTAAACCCAGTGCTGCTGCACCTCCCTAGCGCCTCCTCCCTGCGCGCCCCCGAGG  2220

Qy  2221  AGCATCCCTTAACAAGGCCACCTCCCACGCGGCCTCCACGTCCCAGGAGAGTCGCCGGGAGG  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  AGCATCCCTTAACAAGGCCACCTCCCACGCGGCCTCCACGTCCCAGGAGAGTCGCCGGGAGG  2280

Qy  2281  CCCCCAAGCCCGAGTCTTCCAAGCCTCACAGCGGCCTGCAGCTGCCT  2340
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  CCCCCAAGCCCGAGTCTTCCAAGCCTCACAGCGGCCTGCAGCTGCCT  2340

Qy  2341  GCCTCGCTTCCCGTGAATCGTCCCGTGAATCTGAGCTGGAGACTCCTTGGCTTCCAGGCT  2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  GCCTCGCTTCCCGTGAATCGTCCCGTGAATCTGAGCTGGAGACTCCTTGGCTTCCAGGCT  2400

Qy  2401  CCAGAAAGGAAATGGAGAGGGAAATGGGAAATCTGGAGAGGTGGGGACTGCAGCAGTGTTTC  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  CCAGAAAGGAAATGGAGAGGGAAATGGGAAATCTGGAGAGGTGGGGACTGCAGCAGTGTTTC  2460

Qy  2461  CTCAGAGGGAAAGGGGCCTTCCCACGTCCCAGGAGAATTCCAGGAGGTGGGGACTGGGGAG  2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  CTCAGAGGGAAAGGGGCCTTCCCACGTCCCAGGAGAATTCCAGGAGGTGGGGACTGGGGAG  2520

Qy  2521  TGGGGACGCTGGGGCTGAGCGCGGGTGCTGAAAAGGCTGCTGAAAAGGGCAAGGCTGAA  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  TGGGGACGCTGGGGCTGAGCGCGGGTGCTGAAAAGGCTGCTGAAAAGGGCAAGGCTGAA  2580
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Qy  2581  GCTGCCCAGATGTTGTTCAGTGTTGTTCACGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC  2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  GCTGCCCAGATGTTGTTCAGTGTTGTTCACGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC  2640

Qy  2641  CTTTTATCTTTCTCTGCTTGGAGGAGAAGAGTCTATTTCATGAAGGATGCAGTTTC  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  CTTTTATCTTTCTCTGCTTGGAGGAGAAGAGTCTATTTCATGAAGGATGCAGTTTC  2700

Qy  2701  ATAAAGTCAGCTGTTAAAATTCCAGGTGTGCATGGGTTTCCTTCACGAAGGCCTTTAT  2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  ATAAAGTCAGCTGTTAAAATTCCAGGTGTGCATGGGTTTCCTTCACGAAGGCCTTTAT  2760

Qy  2761  TTAATGGAATATAGGAAGGAGCCGTCATTTCCTAGGCGTTAATTCCACGGAGAAGTGAC  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  TTAATGGAATATAGGAAGGAGCCGTCATTTCCTAGGCGTTAATTCCACGGAGAAGTGAC  2820

Qy  2821  TGGAGTCTTTTCTTCATGTCTTCTGGGCAACTACTCAGCCCGTGTGGACTTGGCTTA  2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  TGGAGTCTTTTCTTCATGTCTTCTGGGCAACTACTCAGCCCGTGTGGACTTGGCTTA  2880

Qy  2881  TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTCTTCTGGTTCTGCCATT  2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTCTTCTGGTTCTGCCATT  2940

Qy  2941  GGTTGGCTGTGCGACCGTGGACCGTGCGCAAGTGTCTCCGTTCCTGAACACTTCCCTGGGGG  3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  GGTTGGCTGTGCGACCGTGGACCGTGCGCAAGTGTCTCCGTTCCTGAACACTTCCCTGGGGG  3000

Qy  3001  ATAAAGACCCTTGCAGCTCCGTGTTCGTGGTTCTCCGTTCCCTGATTCCGTGTGGGGG  3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  ATAAAGACCCTTGCAGCTCCGTGTTCGTGGTTCTCCGTTCCCTGATTCCGTGTGGGGG  3060

Qy  3061  GGATGTTGAGAGGGAAGGACAGGAGCAGTGAGCAGCTGAGCCTCCTCACGTCAGACTC  3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  GGATGTTGAGAGGGAAGGACAGGAGCAGTGAGCAGCTGAGCCTCCTCACGTCAGACTC  3120

Qy  3121  GGACAGGAAGGCAGGCGAGAAGCGCAATGCATTGCAATAACCAAAAGAATGCAGAGATGGT  3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  GGACAGGAAGGCAGGCGAGAAGCGCAATGCATTGCAATAACCAAAAGAATGCAGAGATGGT  3180

Qy  3181  CAGGACCATAGACAATGCATTGCTTCAGGAAAGCTCAATGAACCCAAGAAAGCAGCCACATTTTCCT  3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181  CAGGACCATAGACAATGCATTGCTTCAGGAAAGCTCAATGAACCCAAGAAAGCAGCCACATTTTCCT  3240

Qy  3241  TCCCTAAGCATGACAATTGGGCGCCCCTCAAAACTGGGAAAAATGCGAAGTGAAAATGCAGAGATTG  3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  TCCCTAAGCATGACAATTGGGCGCCCCTCAAAACTGGGAAAAATGCGAAGTGAAAATGCAGAGATTG  3300

Qy  3301  GGTAGCTTTTGCTGGCATTCAAAAACTGGGAGGTGGGGACTGCAAGTGAAAATGCCAGAGATTG  3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301  GGTAGCTTTTGCTGGCATTCAAAAACTGGGAGGTGGGGACTGCAAGTGAAAATGCCAGAGATTG  3360

Qy  3361  TTAAACTTTTCACCCTGACCAGCAGCTCAGCAGTCTGACTGCTCAGCTGTGACACGCACG  3420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361  TTAAACTTTTCACCCTGACCAGCAGCTCAGCAGTCTGACTGCTCAGCTGTGACACGCACG  3420

Qy  3421  AGTGACCTGCAGCGCAGGCAGGGGAGAGAGAAAGAGAGGGGATGAGTAGTGTGGAGCAAGAAAG  3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421  AGTGACCTGCAGCGCAGGCAGGGGAGAGAGAAAGAGAGGGGATGAGTAGTGTGGAGCAAGAAAG  3480

Qy  3481  ACAGATTCATTCAAGGGCAGGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGTGTTTC  3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481  ACAGATTCATTCAAGGGCAGGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGTGTTTC  3540

Qy  3541  GTTCTAGGAGGCAGGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGTCGGGAGA  3600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541  GTTCTAGGAGGCAGGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGTCGGGAGA  3600

Qy  3601  CCTGATTTCTAATACTATATTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGGCTCACAAG  3660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601  CCTGATTTCTAATACTATATTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGGCTCACAAG  3660
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Qy    3661 GTAGTAACTGAGGCTGTAAGATTACTACTTAGTTTCTCCTTATTAGGAACTCTTTTTTCTCTGT 3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3661 GTAGTAACTGAGGCTGTAAGATTACTACTTAGTTTCTCCTTATTAGGAACTCTTTTTTCTCTGT 3720

Qy    3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTCTTTTAACAGGAAGAAAAACATTCCTAAGAG 3780
           |||||||||||||||||||||||||||| |||||| || |||||||||||||||||||||||||
Db    3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAAACATTCCTAAGAG 3780

Qy    3781 TAAAGCCAAACACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3781 TAAAGCCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTTGAAAAAT 3840

Qy    3841 CATTTCAGCGATGTTACTATCTGATTCAGAAAATGAGACTAGTACCCCTTTGGTCAGCTG 3900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3841 CATTTCAGCGATGTTACTATCTGATTCAGAAAATGAGACTAGTACCCCTTTGGTCAGCTG 3900

Qy    3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 3960

Qy    3960 AAGAATAGGAACATTATTATTGGGATGGGTGCATAAATTGGGATGTTCTTTAAAAAGA 4019
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3961 AAGAATAGGAACATATTATTGGGATGGGTGCATAAATTGGGATGTTCTTTTAAAAAGA 4019

Qy    4020 CAGTTTGGAAATATTACTTCACAAGTAGTTGACACTGTTGGTATTAACAACATAAAG 4079
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4020 CAGTTTGGAAATATTACTTCACAAGTAGTTGACACTGTTGGTATTAACAACATAAAG 4079

Qy    4080 TTGCTCAAAGGCAATCATTATTTCAAGTAGCTTAAAGTAGCTTTGGTATA 4139
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4080 TTGCTCAAAGGCAATCATTATTTCAAGTAGCTTAAAGTAGCTTTGGTATA 4139

Qy    4140 TTTATTGGCTATTGCCATTTGCTTTTGTTTTTTGGGTTTATTAAATGTAAAGCA 4199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4140 TTTATTGGCTATTGCCATTTGCTTTTGTTTTTTGGGTTTATTAAATGTAAAGCA 4199

Qy    4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTGAAATTGAAGGAAAAATTACATTT 4259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTGAAATTGAAGGAAAAATTACGTTT 4259

Qy    4260 TTGTTTTTTACCACCTTCTAACTAAATTTAATTAAATTTATTCCATTGCGAATAGAGCCATAA 4319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4260 TTATTTTTACCACCTTCTAACTAAATTTAATTAAATTTATTCCATTGCGAATAGAGCCATAA 4319

Qy    4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
           |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4320 ACTCAAAGTGGTAATAAGAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379

Qy    4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTTCAAAACT 4439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTTCAAAACT 4439

Qy    4440 ACTTTGAAATTAGACCTCCCGCTGGATCCTGTGTTTTTAACATAAAAACATGTTTAA 4499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4440 ACTTTGAAATTAGACCTCCCGCTGGATCCTGTGTTTTTAACATAAAAACATGTTTAA 4499

Qy    4500 AATTTTGATATTTGATAATCATATTTGTTTCCTTTGTAATCTATATTT 4559
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    4500 AATTTTGATATTTGATAATCATATTTGTTTCCTTTGTAATCTATATTT 4559

Qy    4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCCAATGAGGTTCTTG 4619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCCAATGAGGTTCTTG 4619

Qy    4620 GCATGCACACACAGAGTAAGAACTGATTTAGAGGGTAACATTGACATTGGTTGGTGCCTGAG 4679
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4620 GCATGCACACACAGAGTAAGAACTGATTTAGAGGGTAACATTGACATTGGTTGGTGCCTGAG 4679

Qy    4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACAGTTGTTTTAAAGCTAGGGGT 4739
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACAGTTGTTTTAAAGCTAGGGGT 4739

Qy    4740 GAGGGGGGAAATCTGCCGCTGGCTGGCTCTATAGGAATGCTCTCCCGTCCCTGGGAGCCTACGTCTGTGT 4799
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4740 GAGGGGGGAAATCTGCCGCTGGCTGGCTCTATAGGAATGCTCTCCGTCCCTGGGAGCCTACGTCTTAAAGGACTTGTT 4799
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Db    4740 GAGGGGGGAAATCTGCCGCTGGCTGGCTCTATAGGAATGCTCTCCGTCCCTGGGAGCCTACGTCTTAAAGGACTTGTT 4799

Qy    4800 CCTTGTGTTCTCGGCTGGCTGTATTTTCTCTGTCCCGTCCCTGGGAGCCTACGTCTTAAAGGACTTGTT 4859
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4800 CCTTGTGTTCTCGGCTGGCTGTATTTTCTCTGTCCCGTCCCTGGGAGCCTACGTCTTAAAGGACTTGTT 4859

Qy    4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGCGCACAGTCGCAGTTCTCAATGAGTTTGCAGA 4919
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGCGCACAGTCGCAGTTCTCAATGAGTTTGCAGA 4919

Qy    4920 GTGAATGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACCAGTAGTCCTG 4979
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4920 GTGAATGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACCAGTAGTCCTG 4979

Qy    4980 GTGTAAGTGTGTGTAC----GTGTGTGTGTGTGTGTAAAACCAGGTGG 5035
           ||||||||||||||||    ||||||||||||||||||||||||||||
Db    4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGG 5039

Qy    5036 AGATATAGGAACTATTATTGGGATGGGTGCATAAATTGGGATGTTCTTTTAAAAAGA 5095
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5040 AGATATAGGAACTATTATTGGGATGGGTGCATAAATTGGGATGTTCTTTTAAAAAGA 5099

Qy    5096 AACTCCAAACAGACTTCTGGAAGTTATTTCTAAGAATCTTGCTGGCAGCCGCGTGAAGGCA 5155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5100 AACTCCAAACAGACTTCTGGAAGTTATTTCTAAGAATCTTGCTGGCAGCCGCGTGAAGGCA 5159

Qy    5156 ACCCCCCTGCACAGCCCCACCTGGCCACCTCTGTCTTCCCCATGAAG 5215
           |||||||||||||||||||||||||||||||||||||||||||||||
Db    5160 ACCCCCCTGCACAGCCCCACCTGGCCACCTCTGTCTTCCCCATGAAG 5219

Qy    5216 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5220 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5275
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RESULT 7
US-09-306-828-2
; Sequence 2, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 2
; LENGTH: 5304
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-2

Query Match   99.1%; Score 5224.4; DB 3; Length 5304;
Best Local Similarity 99.8%;
Matches 5264; Conservative 0; Mismatches 0; Indels 6; Gaps 3;

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Qy       1 ATCTTTGTTCAGTTTACCTCAGGCCTATTCGGATGATAAGATAAGAATCA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATCTTTGTTCAGTTTACCTCAGGCCTATTCGGATGATAAGATAAGAATCA 60

Qy      61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAAGAATCA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAAGAATCA 120

Qy     121 GGAAGAAGGAGTATCCACGTTAGCCACGTGTCTCAGGCGTGTGTCTATTTTAGTGA 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GGAAGAAGGAGTATCCACGTTAGCCACGTGTCTCAGGCGTGTGTCTATTTTAGTGA 180
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Qy  1261 TACAGCCAGAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTACCTGTATGCTCTAC 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 TACAGCCAGAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTACCTGTATGCTCTAC 1320

Qy  1321 ACCTGAGCTCACTGCAACCTCTGCCTTCGCCTCTGCCTTCAGGTTCAAGCAATTCTCCGTCTCAGCCTCC 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 ACCTGAGCTCACTGCAACCTCTGCCTTCGCCTCTGCCTTCAGGTTCAAGCAATTCTCCGTCTCAGCCTCC 1380

Qy  1381 CGCGTAGCTGGGACTACAGGCGCACCGCCCGGCACCGCCCGGCTAATTTTGTATTGTTAGTAGAGATGGG 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CGCGTAGCTGGGACTACAGGCGCACCGCCCGGCACCGCCCGGCTAATTTTGTATTGTTAGTAGAGATGGG 1440

Qy  1441 GTTTCACCATATTAGCCCGGGCTGGTCTTGAACTCCTGACCTCAGGTGATCACCCACCTC 1500
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Db  1441 GTTTCACCATATTAGCCCGGGCTGGTCTTGAACTCCTGACCTCAGGTGATCACCCACCTC 1500

Qy  1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
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Db  1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560

Qy  1561 TTAATAAGGAATAACTTGATTGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 TTAATAAGGAATAACTTGATTGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620

Qy  1621 TAATTTCAGGGATTCTTGGGATGGGAATGGTGCCATGAGTGCCTGCCTAGTCCCAGAC 1680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 TAATTTCAGGGATTCTTGGGATGGGAATGGTGCCATGAGTGCCTGCCTAGTCCCAGAC 1680

Qy  1681 CACTGGTCCTCATCACTTCTTCCTCCATCCTCATTTTCAGGCTAAGTACCATTTTATT 1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 CACTGGTCCTCATCACTTCTTCCTCCATCCTCATTTTCAGGCTAAGTACCATTTTATT 1740

Qy  1741 CACCATGCTTTTGTGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
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Db  1741 CACCATGCTTTTGTGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy  1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGGGACGAGGGCATACCCCAGACTCCT 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGGGACGAGGGCATACCCCAGACTCCT 1860

Qy  1861 TGAAGCCCCGGCAGAGTTTCCTCGCAGCAGCGTGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 TGAAGCCCCGGCAGAGTTTCCTCGCAGCAGCGTGGGGAGCCCTGCAAGCACCCGGGGTCC 1920

Qy  1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTGTTGTTTGTTATCACTCTCTAGG 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTGTTGTTTGTTATCACTCTCTAGG 1980

Qy  1981 GACCTGTTGCTTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 GACCTGTTGCTTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy  2041 TATTGAGTACTTATATCTGCCAGACACCAGACAAATGGTGAGCAAAGAGTCACTGC 2100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 TATTGAGTACTTATATCTGCCAGACACCAGACAAATGGTGAGCAAAGAGTCACTGC 2100

Qy  2101 CCTACCTTCGTGGAGTGACAGTTTCTCATGAAGACGTGAGAAGAAAATTAATAGCA 2160
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Db  2101 CCTACCTTCGTGGAGTGACAGTTTCTCATGAAGACGTGAGAAGAAAATTAATAGCCA 2160

Qy  2161 GCCAACTTAAACCCAGTGCTACAAGGCGAAAGAAAGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCCAACTTAAACCCAGTGCTACAAGGCGAAAGAAAGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy  2221 AGGATCCCTTAACAAGGCCACCTCGCCTCCCATCGTGCCCGGAG 2280
         ||||||||||||||||||||||||||||||||||||||||||||
Db  2221 AGGATCCCTTAACAAGGCCACCTCGCCTCCCATCGTGCCCGGAG 2280

Qy  2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCCACTCGAGCTGGCCT 2340
         |||||||||||||||||||||||||||||||||||||||||||
Db  2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCCACTCGAGCTGGCCT 2340

Qy  2341 GCCTCGCTTCCCGTGAATCGTCCGGTCGATCGTGAGCTGGAGACTCCTTGGCTCCAGCT 2400
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Qy  181  CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy  241  CATCAAAACAGGAGCTAAGAAACAGGAATGAGAATGGGCACTTGCCCAAGGAAAATGCCAG 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  CATCAAAACAGGAGCTAAGAAACAGGAATGAGAATGGGCACTTGCCCAAGGAAAATGCCAG 300

Qy  301  GAGAGCAAATAATGATGAAAATAAACTTTCCCTTTGTGTTTAATTTCAGGAAAAAATG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  GAGAGCAAATAATGATGAAAATAAACTTTCCCTTTGTGTTTAATTTCAGGAAAAAATG 360

Qy  361  ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTGTTCCAAATTGG 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTGTTCCAAATTGG 420

Qy  421  TAATTAAGTATTTGTTCCTTGGGAAGACCTTCATGTGAGCTTGATGGGAAAATGGGAA 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  TAATTAAGTATTTGTTCCTTGGGAAGACCTTCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy  481  AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy  541  GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAGGACATAACAATAAC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAGGACATAACAATAAC 600

Qy  601  AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGACTGGGAAAGCTTCATAAC 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGACTGGGAAAGCTTCATAAC 660

Qy  661  AGTGATTAGGCAGTTGACCATGTTCGGCAACACTCCCGTCTATACCAGGAACACAAAA 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  AGTGATTAGGCAGTTGACCATGTTCGGCAACACTCCCGTCTATACCAGGAACACAAAA 720

Qy  721  ATTGACTGGGCTAAGCTGGACTTTCAAGGAGAAATGAAAAACTGAGAGACAAACAAAA 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721  ATTGACTGGGCTAAGCTGGACTTTCAAGGAGAAATGAAAAACTGAGAGACAAACAAAA 780

Qy  781  GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781  GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy  841  GGGACCCTGAGGCATTGCCTTTAGGAGGCCAGTTTCTTAAGGAATCTTAAGAAACTC 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841  GGGACCCTGAGGCATTGCCTTTAGGAGGCCAGTTTCTTAAGGAATCTTAAGAAACTC 900

Qy  901  TTGAAGATCATGAATTTAACCATTTTAAGTATAAAAACAAATATGCGATGCATAATCAG 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901  TTGAAGATCATGAATTTAACCATTTTAAGTATAAAAACAAATATGCGATGCATAATCAG 960

Qy  961  TTTAGACATGGCTCCCAATTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961  TTTAGACATGGCTCCCAATTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy  1021 GGATAGGTCAGAAATCATTAGAATCACTGTGTCCCATCTTTTTCAGAATGATC 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGATAGGTCAGAAATCATTAGAATCACTGTGTCCCATCTTTTTCAGAATGATC 1080

Qy  1081 TGTCATAGCCCTCACACACAGCGCCCGATGTGTCGACCATCTACAACCCAA 1140
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Db  1081 TGTCATAGCCCTCACACACAGCGCCCGATGTGTCGACCATCTACAACCCAA 1140

Qy  1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCATTACAAATGCCACCTCCC 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCATTACAAATGCCACCTCCC 1200

Qy  1201 TGTGCAGCCCATCCCGCTCCACAGGAGCTCTCCCACTCTGCATCACGATGT 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 TGTGCAGCCCATCCCGCTCCACAGGAGCTCTCCCACTCTGCATCACGATGT 1260
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Db  2341  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  2400
          GCCTTCGCTTCCCGTGAATGTCTTGGTCGATCTGAGCTGGAGAACTGGCTCCAGGCT

Qy  2401  CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGATCTGAGCGAGAGGGAAACTGGCTCCAGGCT  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGATCTGAGCGAGAGGGAAACTGGCTCCAGGCT  2460

Qy  2461  CTCAGAGGGGAAAGGGGCCTTCCAGTCCCAGGAGAATTCAGGAGGTGGGGACTGGGAGGCGCAGGGAG  2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  CTCAGAGGGGAAAGGGGCCTTCCAGTCCCAGGAGAATTCAGGAGGTGGGGACTGGGAGGCGCAGGGAG  2520

Qy  2521  TGGGGACCGCTGGGCGCTGGGCGCTGGGGCTGAGCGCGGGTGCTGAAAGGGGCTGAAAGGGGCAAGGG  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  TGGGGACCGCTGGGCGCTGGGCGCTGGGGCTGAGCGCGGGTGCTGAAAGGGGCTGAAAGGGGCAAGGG  2580

Qy  2581  GCTGCCCAGATGTTCAGTTGTTGTTCTGGAGGAGGAGCGAGCTCATTTCCGTTAATTCACGGAAGAAG  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  GCTGCCCAGATGTTCAGTTGTTGTTCTGGAGGAGGAGCGAGCTCATTTCCGTTAATTCACGGAAGAAG  2640

Qy  2641  CTTTTTATCTTTTCTCTGTTGAGGAGAGAGTCTATTTCATGAAGGGATCAGTTTC  2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  CTTTTTATCTTTTCTCTGTTGAGGAGAGAGTCTATTTCATGAAGGGATCAGTTTC  2700

Qy  2701  ATAAAGTCAGCTGTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGGAAGGCCTTTAT  2760
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Db  2701  ATAAAGTCAGCTGTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGGAAGGCCTTTAT  2760

Qy  2761  TTAATGGGAATATAGGAAGCGAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  TTAATGGGAATATAGGAAGCGAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC  2820

Qy  2821  TCGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGGCTTA  2880
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Db  2821  TCGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGGCTTA  2880

Qy  2881  TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCCGTTTCTTTCGGTTCTGCCATT  2940
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Db  2881  TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCCGTTTCTTTCGGTTCTGCCATT  2940

Qy  2941  GGTTGGCTGTGCGACCCGTGGGCAAGTGTCTCGTTCGTTCTGATTCTCTGTGAGGGG  3000
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Db  2941  GGTTGGCTGTGCGACCCGTGGGCAAGTGTCTCGTTCGTTCTGATTCTCTGTGAGGGG  3000

Qy  3001  ATAAAGACCCCTGCAGCTCGTTCCCGTGAATGAACCCAACAGCCCAACATTTTCCT  3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  ATAAAGACCCCTGCAGCTCGTTCCCGTGAATGAACCCAACAGCCCAACATTTTCCT  3060

Qy  3061  GGATGTTGAGAGGGAAGGAGGAGCAGAGTCGAGCCACACAGGGAGGTGGAGGG  3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  GGATGTTGAGAGGGAAGGAGGAGCAGAGTCGAGCCACACAGGGAGGTGGAGGG  3120

Qy  3121  GGACAGGAAGGCAGGCAGCAGGCAGAAGCTGGGTCGTCCATCAGTCCTCAGATCAGACTC  3180
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Db  3121  GGACAGGAAGGCAGGCAGCAGGCAGAAGCTGGGTCGTCCATCAGTCCTCAGATCAGACTC  3180

Qy  3181  CAGGACCGAGAGCCAGAGCCACAAATGCTTCAGGAAAGTCAATGAACCCAACATTTTCCT  3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181  CAGGACCGAGAGCCAGAGCCACAAATGCTTCAGGAAAGTCAATGAACCCAACATTTTCCT  3240

Qy  3241  TCCCTAAGCAATAGACAATGGCATTTGCCAATAACCAAAAGAAGAATGCAGAGACTAACTGGT  3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  TCCCTAAGCAATAGACAATGGCATTTGCCAATAACCAAAAGAAGAATGCAGAGACTAACTGGT  3300

Qy  3301  GGTAGCTTTTGCCTGGCATTCAAAAAACTGGGCCAGACAAGCTCAGAAATGCCAGAGATTG  3360
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Db  3301  GGTAGCTTTTGCCTGGCATTCAAAAAACTGGGCCAGACAAGCTCAGAAATGCCAGAGATTG  3360

Qy  3361  TTAAACTTTTCACCCTGACCAGCACCCCACCACGAGCTCGACTGCTGACAGCACGCGG  3420
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Db  3361  TTAAACTTTTCACCCTGACCAGCACCCCACCACGAGCTCGACTGCTGACAGCACGCGG  3420

Qy  3421  AGTGACCTGCAGCCAGGGGAGGAGAAAGAGAGGGATAGTGTATGAGCAAGAAAG  3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421  AGTGACCTGCAGCCAGGGGAGGAGAAAGAGAGGGATAGTGTATGAGCAAGAAAG  3480

Qy  3481  ACAGATTCATTCAAGGGCAGTGGGAATTGACCCACGGATTATAGTCCCACGTGATCCTGG  3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481  ACAGATTCATTCAAGGGCAGTGGGAATTGACCCACGGATTATAGTCCCACGTGATCCTGT  3540

Qy  3541  GTTCTAGGAGGCAGGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAGTCGGGAGA  3600
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541  GTTCTAGGAGGCAGGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAGTCGGGAGA  3600

Qy  3601  CCTGATTTCTAATACTATATTTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG  3660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601  CCTGATTTCTAATACTATATTTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG  3660

Qy  3661  GTAGTAACTGAGCGTGTAAGAATTACTTAGTTCTCCTTATTAGGAACTCTTTTCTCTGT  3720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661  GTAGTAACTGAGCGTGTAAGAATTACTTAGTTCTCCTTATTAGGAACTCTTTTCTCTGT  3720

Qy  3721  GGAGTTAGCAGCACAAGGGCAATCCGTTCTTTCTTTAACAGGAAGAAACATTCCTAAGAG  3780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721  GGAGTTAGCAGCACAAGGGCAATCCGTTCTTTCTTTAACAGGAAGAAACATTCCTAAGAG  3780

Qy  3781  TAAAGCCAAACAGATTCAAGCCTAGGTCTGCTAGCCTAGGTCTGCTGACTATGATTGTTTTGAAAAAT  3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781  TAAAGCCAAACAGATTCAAGCCTAGGTCTGCTAGCCTAGGTCTGCTGACTATATGATTGTTTTGAAAAAT  3840

Qy  3841  CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTGGTCAGCTG  3900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841  CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTGGTCAGCTG  3900

Qy  3901  TAAACAAACACCCAGTGTAAATGTCTCAAGTCAGGCTAACTGCAGAACCAATCAA-  3959
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Db  3901  TAAACAAACACCCAGTGTAAATGTCTCAAGTCAGGCTAACTGCAGAACCAATCAAAT  3960

Qy  3960  AAGAATAGAATCTTAGAGCAAACTGTGTTCCACTGTGTTGGTATTAACAACATAAAAGGGG  4019
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db  3961  AAGAATAGAATCTTAGAGCAAACTGTGTTCCAC-TCTGGAGGTGAGTCTGCCCAGGGG  4019

Qy  4020  CAGTTTGGAAATATTACTTCACAAGTATTGCACACTGTTGTTGGTATTAACAACATAAAG  4079
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4020  CAGTTTGGAAATATTACTTCACAAGTATTGCACACTGTTGTTGGTATTAACAACATAAAG  4079

Qy  4080  TTGCTCAAAGGCAATCATTATTTCAAGTGCTTAAAGTTACTTCTGACAGTTTTGGTATA  4139
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4080  TTGCTCAAAGGCAATCATTATTTCAAGTGCTTAAAGTTACTTCTGACAGTTTTGGTATA  4139

Qy  4140  TTTATTGGCTATTGCCATTTGCTTTTGTTTTGTCTCTTTGGGTTTATTAATGTAAAGCA  4199
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4140  TTTATTGGCTATTGCCATTTGCTTTTGTTTTGTCTCTTTGGGTTTATTAATGTAAAGCA  4199

Qy  4200  GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTGAATGAGGAAAAATTACATTTT  4259
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4200  GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTGAATGAGGAAAAATTACGTTTT  4259

Qy  4260  TTGTTTTTACCACCTTCTAACTAAATTTAATTTATTCCATTGCCAATAGAGCCATAA  4319
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Db  4260  TTATTTTTACCACCTTCTAACTAAATTTAATTTATTCCATTGCCAATAGAGCCATAA  4319

Qy  4320  ACTCAAAGTGGTAATAACAGTACCTGTGATTTGTGTAGTTCATTCCAATCACAGACAT  4379
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Db  4320  ACTCAAAGTGGTAATAACAGTACCTGTGATTTGTGTAGTTCATTCCAATCACAGACAT  4379

Qy  4380  TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTTATACTTCAAAACT  4439
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Db  4380  TTTATACTATATTACAGTTGTTGCAGGTACGTTGTAAGTGAAATATTTTATACTCAAAACT  4439

Qy  4440  ACTTTGAAATTTAGACCTTCCTGATCTTGTTTTTTAACATATTTAATAAAACATGTTTAA  4499
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Db  4440  TTATTTGAAATTTAGACCTTCCTGATCTTGTTTTTTAACATATTTAATAAAACATGTTTAA  4499

Qy  4500  AATTTTGATATTTGATAATCATATTTCATTATCATTTGTTTTCCTTTGTTAATCTATATTT  4559
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Db  4500  AATTTTGATATTTGATAATCATATTTCATTATCATTTGTTTTCCTTTGTTAATCTATATTT  4559
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CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/056,285A
 FILING DATE: 07-Apr-1998
 ATTORNEY/AGENT INFORMATION:
  NAME: Arnold, Beth E.
  REGISTRATION NUMBER: 35,430
  REFERENCE/DOCKET NUMBER: UIA-010.28
 TELECOMMUNICATION INFORMATION:
  TELEPHONE: 617-832-1000
  TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
  LENGTH: 2800 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-056-285A-1

Query Match   34.2%;   Score 1804.4;   DB 3;   Length 2800;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 1838;   Conservative   0;   Mismatches   0;   Indels   1;   Gaps   3;

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Qy  3431 AGGCGCAGGGAGGAGGAGAAGAAAAAGAGAGGGATAGTAGTGTATGAGCAAGAAAGACAGATTCAT 3490
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Db     1 AGGCGCAGGGAGGAGGAGAAG-AAAGAGAGGGATAGTAGTGTATGAGCAAGAAAGACAGATTCAT   59

Qy  3491 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 3550
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    60 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG  119

Qy  3551 GCAGGGCTATATTGTGGGGGGCGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 3610
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   120 GCAGGGCTATATTGTGGGGGGCGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT  179

Qy  3611 AATACTATATTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 3670
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Db   180 AATACTATATTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG  239

Qy  3671 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTCTCTGTGGAGTTAGCA 3730
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   240 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTCTCTGTGGAGTTAGCA  299

Qy  3731 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 3790
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA  359

Qy  3791 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTGAAAAATCATTTCAGCG 3850
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Db   360 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTGAAAAATCATTTCAGCG  419

Qy  3851 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 3910
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   420 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA  479

Qy  3911 CCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA-AAGAATAGAA 3969
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Db   480 CCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAATAAGAATAGAA  539

Qy  3970 TCTTTAGAGCAAACTGGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGGCAGTTTCGGAA 4029
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Db   540 TCTTTAGAGCAAACTGGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGGGCAGTTTCGGAA  598

Qy  4030 ATATTTACTTCACAAGTATTGACACTGTTGGTATTAACACATAAAGTTGCTCAAAG 4089
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   599 ATATTTACTTCACAAGTATTGACACTGTTGGTATTAACACATAAAGTTGCTCAAAG  658

Qy  4090 GCAATCATTATTTCAAGTGGCTTAAAGTACTTCTGACAGTTTGTATATTTATTGGCT 4149
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Db   659 GCAATCATTATTTCAAGTGGCTTAAAGTACTTCTGACAGTTTGTATATTTATTGGCT  718

Qy  4150 ATTGCCATTGCTTTGTTTTTCTCTTGGGTTTATTAATGTAAAGCAGGGATTATTA 4209
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Qy  4560 TATATATTTGAAAACATCTTCTGAGAAGAGTTCCCAGATTTCACCAATGAGGTTCTTG 4619
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Db  4560 TATATATTTGAAAACATCTTCTGAGAAGAGTTCCCAGATTTCACCAATGAGGTTCTTG 4619

Qy  4620 GCATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
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Db  4620 GCATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679

Qy  4680 ATGCAAGACTGAAATAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGGT 4739
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4680 ATGCAAGACTGAAATAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGGT 4739

Qy  4740 GAGGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCCCCTGGTAGGGTGCTGT 4799
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4740 GAGGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCCCCTGGTAGGGTGCTGT 4799

Qy  4800 CCTTGTGTTCTGGCTGGCTGGCTGTTATTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4800 CCTTGTGTTCTGGCTGGCTGGCTGTTATTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859

Qy  4860 TGGATCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4860 TGGATCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919

Qy  4920 GTGAATGGAAATATAAAACTAGAAATATCTTGTTGAAATCAGCAGCACCAGTAGTCCTG 4979
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Db  4920 GTGAATGGAAATATAAAACTAGAAATATCTTGTTGAAATCAGCAGCACCAGTAGTCCTG 4979

Qy  4980 GTGTAAGTGTGTGTAC---GTGTGTGTGTGTGTGTAAAACCAGGTGG 5035
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Db  4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGG 5039

Qy  5036 AGATATAGGAACTATTATTGGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGA 5095
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5040 AGATATAGGAACTATTATTGGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGA 5099

Qy  5096 AACTCCAAACAGACTTCTGAAGGTTATTTTCTAAGAATCTTGCTGCTGGCAGCGTGAAGGCA 5155
         |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db  5100 AACTCCAAACAGACTTCTGAAGGTTATTTTCTAACAATCTTGCTGCTGGCAGCGTGAAGGCA 5159

Qy  5156 ACCCCCTGTGCACAGCCCCACCCCCACCCCCTGTCTTCTTCCCCATGAGAG 5215
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Db  5160 ACCCCCTGTGCACAGCCCCACCCCCACCCCCTGTCTTCTTCCCCATGAGAG 5219

Qy  5216 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGCATGAGCCAGCAAGG 5271
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5220 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGCATGAGCCAGCAAGG 5275
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RESULT 8
US-09-056-285A-1
; Sequence 1, Application US/09056285A
; Patent No. 6403307
 GENERAL INFORMATION:
  APPLICANT: Stone, Edwin M.
             Sheffield, Val C.
             Alward, Wallace L.M.
             Fingert, John
  TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
  NUMBER OF SEQUENCES: 43
  CORRESPONDENCE ADDRESS:
   ADDRESSEE: FOLEY, HOAG & ELIOT LLP
   STREET: One Post Office Square
   CITY: Boston
   STATE: MA
   COUNTRY: USA
   ZIP: 02109-2170
  COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE: PatentIn Release #1.0, Version #1.30

Db   1799 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAGG 1840

RESULT 9
US-10-017-870-10
; Sequence 10, Application US/10017870
; Patent No. 6727354
; GENERAL INFORMATION:
;   APPLICANT: HUANG, DOUG HUI
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TIGR GENOTYPING ASSAYS
;   FILE REFERENCE: 034827-1401
;   CURRENT APPLICATION NUMBER: US/10/017,870
;   CURRENT FILING DATE: 2001-12-12
;   NUMBER OF SEQ ID NOS: 14
;   SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 10
;   LENGTH: 2800
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-017-870-10

Query Match   34.2%;   Score 1804.4;   DB 3;   Length 2800;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 1838;   Conservative   0;   Mismatches   0;   Indels   3;   Gaps   3;

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Qy  3431 AGCGCAGGGAGGAGAGAAAAGAGACGGATAGTGTATGAGCAAGAAGACAGATTCAT 3490
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Qy  3491 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 3550
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Db    60 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 119

Qy  3551 GCAGGGCTATATTGTGGGGGGAAAAATCAGTTCAAGGGAGTCGGGAGACCTGATTCT 3610
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Db   120 GCAGGGCTATATTGTGGGGGGAAAAATCAGTTCAAGGGAGTCGGGAGACCTGATTCT 179

Qy  3611 AATACTATATTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGGTAGTAACTG 3670
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Db   180 AATACTATATTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGGTAGTAACTG 239

Qy  3671 AGGCTGTAAGATTACTTAGTTTCTCCTTATAGGAGAACTCTTTTCTCTGTGGAGTTAGCA 3730
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Db   240 AGGCTGTAAGATTACTTAGTTTCTCCTTATAGGAGAACTCTTTTCTCTGTGGAGTTAGCA 299

Qy  3731 GCACAAGGCAATCCCGTTCTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 3790
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Db   300 GCACAAGGCAATCCCGTTCTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 359

Qy  3791 CAGATTCAAGCCTAGTCTTGCTGACTATATGATTGGTTTTTGAAAAATCATTTCAGCG 3850
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Db   360 CAGATTCAAGCCTAGTCTTGCTGACTATATGATTGGTTTTTGAAAAATCATTTCAGCG 419

Qy  3851 ATGTTTACTATCTGATTCAGAAAATGACTAGTACCCTTGGTCAGCTGTAAACAAACA 3910
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Db   420 ATGTTTACTATCTGATTCAGAAAATGACTAGTACCCTTGGTCAGCTGTAAACAAACA 479

Qy  3911 CCCAGTTGTAAATGCTCAAGTTCAGGCTCAGCCAACCAATCAA-AGAAATAGAA 3969
         ||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   480 CCCATTTGTAAATGTCCAAGTTCAGGCTCAGCCAACCAATCAAATAAGAATAGAA 539

Qy  3970 TCTTTAGAGCAAACTGTGTTCTCCCATCTGAGCGTGAGTCTTGAA 4029
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Db   540 TCTTTAGAGCAAACTGTGTTTCTCCCAC-TCTCGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 598

Qy  4030 ATATTTACTTCACAACTATTGACACTGTTGGTATTAACACATAAAGTTGCTCAAAG 4089
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   599 ATATTTACTTCACAACTATTGACACTGTTGGTATTAACACATAAAGTTGCTCAAAG 658

Qy  4090 GCAATCATTATTTCAAGTGGCTTAAAGTACTTCTGACAGTTTGTATATTTATTGGCT 4149
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   659 GCAATCATTATTTCAAGTGGCTTAAAGTACTTCTGACAGTTTGTATATTTATTGGCT 718
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Db   719 ATTGCCATTGCTTTTGTTTTCTCTTGGGTTATTAATGTAAAGCAGGGATTATTA 778

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Qy  4210 ACCTACAGTCCAGAAAGCCTGTGAATTGAATGAGGAGAAAAATTACATTTTGTTTTTAC 4269
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Db   779 ACCTACAGTCCAGAAAGCCTGTGAATTGAATGAGGAGAAAAATTACATTTTGTTTTTAC 838

Qy  4270 CACCTTCAACTAAATTAACATTTTATTCATTGCAATAGAGCCATAAACTCAAAGTG 4329
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Db   839 CACCTTCAACTAAATTAACATTTTATTCATTGCAATAGAGCCATAAACTCAAAGTG 898

Qy  4330 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATAGTAT 4389
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Db   899 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATAGTAT 958

Qy  4390 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 4449
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Db   959 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 1018

Qy  4450 TAGACCTCCTGCTGGATCGTTGTTTTTTAACATATTAATAAACATGTTTAAAATTTTGATA 4509
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Db  1019 TAGACCTCCTGCTGGATCGTTGTTTTTTAACATATTAATAAACATGTTTAAAATTTTGATA 1078

Qy  4510 TTTTGATAATCATATTTCATTATCATTTGTTTTCCTTTGTAATCTATATATTTTATATATTTG 4569
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1079 TTTTGATAATCATATTTCATTATCATTTGTTTTCCTTTGTAATCTATATATTTTATATATTTG 1138

Qy  4570 AAAACATCTTTCGAGAAGAGTTCCCCAGATTCACCCAATGAGGTTCTTGGCATGCACAC 4629
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Db  1139 AAAACATCTTTCGAGAAGAGTTCCCCAGATTCACCCAATGAGGTTCTTGGCATGCACAC 1198

Qy  4630 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGCCTGGTGCCTGAGATGCAAGACT 4689
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Db  1199 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGCCTGGTGCCTGAGATGCAAGACT 1258

Qy  4690 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTGGGGTGAGGGGGGAA 4749
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Db  1259 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTGGGGTGAGGGGGGAA 1318

Qy  4750 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCGTGTAGGGTGCTCCTGTCGTTC 4809
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Db  1319 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCGTGTAGGGTGCTCCTGTCGTTC 1378

Qy  4810 TGGCTGGCTGTGTATTTTTCTCTGTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 4869
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Db  1379 TGGCTGGCTGTGTATTTTTCTCTGTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 1438

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Db  1439 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGCAGAGTGAATGGAA 1498

Qy  4930 ATATAAAACTAGAAAATATATCCTTGTTGAAATGGAATGGTTCTTTTTTAAAAAGAAAACTCCAAACAGAC 4989
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1499 ATATAAAACTAGAAAATATATCCTTGTTGAAATCAGCACACCAGCACCACCAGTAGTCCTGTGAAGTGT 1558

Qy  4990 GTGTACGTGTGTGTGTGTGTGTGTGTGTGGGATGGTTCTTTTTAAAAGAAAACCAGGTGGAGATATAGGAACTA 5049
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Db  1559 GTGTACGTGTGTGTGTGTGTGTGTGTGTGGGATGTTTCTTTAAAAGAAAACCAGGTGGAGATATAGGAACTA 1618

Qy  5050 TTATTGGGGTATGGGGTGCATAAAATTGGGATGTTCTTTTTTAAAAAGAAACTCCAAACAGAC 5109
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Db  1619 TTATTGGGGTATGGGGTGCATAAAATTGGGATGTTCTTTTTTAAAAAGAAACTCCAAACAGAC 1678

Qy  5110 TTCTGGAAGGTTATTTTTCTAAGAATCTGCTGGCAGCGTGAAGGCAACCCCGTGTGCAC 5169
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Db  1679 TTCTGGAAGGTTATTTTTCTAAGAATCTGCTGGCAGCGTGAAGGCAACCCCGTGTGCAC 1738

Qy  5170 AGCCCACCCAGCCTCACGTGCCACCTCTGTCTTCCCCCATGCAGGGCTTGGCTCCCCAG 5229
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Db  1739 AGCCCACCCAGCCTCACGTGCCACCTCTGTCTTCCCCCATGCAGGGCTTGGCTCCCCAG 1798

Qy  5230 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
         ||||||||||||||||||||||||||||||||||||||||||
Db     TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG
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Qy    4150  ATTGCCATTTGCTTTTGTTTTCTCTTGGGTTTATTAATGTAAAGCAGGGATTATTA  4209
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Db     719  ATTGCCATTTGCTTTTGTTTTCTCTTGGGTTTATTAATGTAAAGCAGGGATTATTA   778

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Qy    4270  CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG  4329
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Db     839  CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG   898

Qy    4330  GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTATACTAT  4389
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     899  GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTATACTAT   958

Qy    4390  ATTACAGTTGTTGCAGATACGTTGAAGTGAAATATATTATACTCAAAACTACTTTGAAAT  4449
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     959  ATTACAGTTGTTGCAGATACGTTGAAGTGAAATATATTATACTCAAAACTACTTTGAAAT  1018

Qy    4450  TAGACCTCCTGCTGATCTTGTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA  4509
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1019  TAGACCTCCTGCTGATCTTGTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA  1078

Qy    4510  TTTTGATAATCATATTTCATTATCATTTGTTTCCTTGTAATCTATATTTTATATATTTG  4569
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1079  TTTTGATAATCATATTTCATTATCATTTGTTTCCTTGTAATCTATATTTTATATATTTG  1138

Qy    4570  AAAACATCTTTCTGAGAAGAGTTCCCCAGATTCACCAATGAGGTTCTTGGCATGCACAC  4629
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1139  AAAACATCTTTCTGAGAAGAGTTCCCCAGATTCACCAATGAGGTTCTTGGCATGCACAC  1198

Qy    4630  ACACAGAGTAAGAACTGATTTAGAGCTAACATTGACATTGGTCGTGCCTGAGATGCAAGACT  4689
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1199  ACACAGAGTAAGAACTGATTTAGAGCTAACATTGACATTGGTCGTGCCTGAGATGCAAGACT  1258

Qy    4690  GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGAA  4749
            |||||||||||||||||||||||||||||||||||||||||||||||
Db    1259  GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGAA  1318

Qy    4750  ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTCGTGCCTTGTGTTC  4809
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1319  ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTCGTGCCTTGTGTTC  1378
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        Query Match           34.2%;  Score 1804.4;  DB 3;  Length 2800;
        Best Local Similarity  99.8%;  Pred. No. 0;
        Matches 1838;  Conservative  0;  Mismatches  1;  Indels  3;  Gaps  3;
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Db    3431  AGCGCAGGGAGGGAGGGAGAAGAGAAAAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT  3490
            ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db       1  AGCGCAGGGAGGGAGGGAGAAG-AAAAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT    59

Qy    3491  TCAAGGGCAGTGGGAATTGACCACCAGGGATTATAGTCCACGTGATCCGGGTTCTCAGGAG  3550
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      60  TCAAGGGCAGTGGGAATTGACCACCAGGGATTATAGTCCACGTGATCCGGGTTCTCAGGAG   119

Qy    3551  GCAGGGCTATATTGTGGGGGAAAAAATCAGTTCAAGGGAGTCGGGAGACCTGATTTCT  3610
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     120  GCAGGGCTATATTGTGGGGGAAAAAATCAGTTCAAGGGAGTCGGGAGACCTGATTTCT   179

Qy    3611  AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGTCACAAGTAACTG  3670
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     180  AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGTCACAAGTAACTG   239

Qy    3671  AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTCTCGTGGAGTTAGCA  3730
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240  AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTCTCGTGGAGTTAGCA   299

Qy    3731  GCACAAGGGCAATCCCGTTTCTTCTTTTAACAGGAAGAAAAACATTCCTAAGAGTAAAGCCAAA  3790
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300  GCACAAGGGCAATCCCGTTTCTTCTTTTAACAGGAAGAAAAACATTCCTAAGAGTAAAGCCAAA   359

Qy    3791  CAGATTCAAGCCTAGGTCTTGCTACGTATATGATTGGTTTTTGAAAAATCATTTCAGCG  3850
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360  CAGATTCAAGCCTAGGTCTTGCTACGTATATGATTGGTTTTTGAAAAATCATTTCAGCG   419

Qy    3851  ATGTTTACTACTTGGTCATTCAGAAAATGAGACTAGTACCCTTTGGTCATGCTGTAAACAAACA  3910
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420  ATGTTTACTACTTGGTCATTCAGAAAATGAGACTAGTACCCTTTGGTCATGCTGTAAACAAACA   479
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Db    1799  TATATATAAACCTCTCTGAGCTCGGGCATGAGCCAGCAAGG  1840
            |||||||||||||||||||||||||||||||||||||||||
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Qy    4810  TGGCTGGCTGTGTTATTTTTCTCGTCCCGTCACGTCTTAAAGGACTTGTTTGGATCTCCA  4869
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1379  TGGCTGGCTGTGTTATTTTTCTCGTCCCGTCACGTCTTAAAGGACTTGTTTGGATCTCCA  1438

Qy    4870  GTTCCTAGCATAGTGCCTGCACAGTGCAGTTGCAGTTGCAGAGTGAATGGAA  4929
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1439  GTTCCTAGCATAGTGCCTGCACAGTGCAGTTGCAGTTGCAGAGTGAATGGAA  1498

Qy    4930  ATATAAACTAGAAATATATCCTTGTTGTGAAATCAGCAGCACCAGTCCTCGGTGTAAGTGT  4989
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1499  ATATAAACTAGAAATATATCCTTGTTGTGAAATCAGCAGCACCAGTCCTCGGTGTAAGTGT  1558

Qy    4990  GTGTACGTGTGTGTGTGTGTATGGTGCATAAATTGGGATGTTCTTTTAAAAGAAACTCCAAACAGAC  5049
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1559  GTGTACGTGTGTGTGTGTGTGTGTATGGTGCATAAATTGGGATGTTCTTTTAAAAGAAACTCCAAACAGAC  1618

Qy    5050  TTATTGGGGTATGGTGCATAAATTGGGATGTTCTTTTAAAAGAAACTCCAAACAGAC  5109
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1619  TTATTGGGGTATGGTGCATAAATTGGGATGTTCTTTTAAAAGAAACTCCAAACAGAC  1678

Qy    5110  TTCTGGAAGGTTATTTTCTAAGAATCTTGCTCAAGCGTGGCAGCGTGAAGGCAACCCCGTGCAC  5169
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1679  TTCTGGAAGGTTATTTTCTAAGAATCTTGCTCAAGCGTGGCAGCGTGAAGGCAACCCCCGTGCAC  1738

Qy    5170  AGCCCACCCAGCCTCACGTGCCACCTCTGTCTCTCCCCATGAAGGGCTTGGCTCCCCAG  5229
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1739  AGCCCCACCCAGCCTCACGTGCCACCTCTGTCTCTCCCCATGAAGGGCTTGGCTCCCCAG  1798

Qy    5230  TATATATAAACCTCTCTGAGCTCGGGCATGAGCCAGCAAGG  5271
            |||||||||||||||||||||||||||||||||||||||||
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Qy 4990 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAACCAGGTGGAGATATAGGAACTA 5049
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1559 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAACCAGGTGGAGATATAGGAACTA 1618

Qy 5050 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAGAAACTCCAAACAGAC 5109
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1619 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAGAAACTCCAAACAGAC 1678

Qy 5110 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCTGTGCAC 5169
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1679 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCTGTGCAC 1738

Qy 5170 AGCCCCACCCAGCCTCACGTGGCCACCTCGTCTTCCCCATGAAGGGCTGGCTCCCCAG 5229
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1739 AGCCCCACCCAGCCTCACGTGGCCACCTCGTCTTCCCCATGAAGGGCTGGCTCCCCAG 1798

Qy 5230 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
        ||||||||||||||||||||||||||||||||||||||||||
Db 1799 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 1840
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RESULT 11
US-09-306-828-38
; Sequence 38, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 38
; LENGTH: 227
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-38

Query Match 4.3%; Score 227; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.8e-46;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 5045 AACTATTATTGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAA 5104
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 AACTATTATTGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAA 60

Qy 5105 CAGACTTCTGGAAGGTATTTTCTAAGAATCTTGTCTGGCAGCGTGAAGGCAACCCCCTG 5164
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CAGACTTCTGGAAGGTATTTTCTAAGAATCTTGTCTGGCAGCGTGAAGGCAACCCCCTG 120

Qy 5165 TGCACAGCCCCACCCAGCCTCACGTGGCCACCTCGTCTTCCCCATGAAGGGCTGGCTC 5224
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 TGCACAGCCCCACCCAGCCTCACGTGGCCACCTCGTCTTCCCCATGAAGGGCTGGCTC 180

Qy 5225 CCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 227
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RESULT 12
US-09-306-828-37
; Sequence 37, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua

```
Qy 3911 CCCAGTTGTAAATGTCTCAAGGCTTAACTGCAGACCAATCAA-AAGAATAGAA 3969
        |||||| |||||||||||||||||||||||||||||||||||| |||||||||||
Db  480 CCCATTTGTAAATGTCTCAAGTCTCAGGCTTAACTGCAGACCAATCAAATCAAATAAGAATAGAA 539

Qy 3970 TCTTTAGAGCAAACTGTGTTCTCCACATCTCGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 4029
        ||||||||||||||||||||||||||         ||||||||||||||||||||||||||
Db  540 TCTTTAGAGCAAACTGTGTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 598

Qy 4030 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 4089
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  599 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 658

Qy 4090 GCAATCATTATTTCAAGTGGCTAAAGTTACTTCTGACAGTTTGGTATATTATTGCTCAAAG 4149
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  659 GCAATCATTATTTCAAGTGGCTAAAGTTACTTCTGACAGTTTGGTATATTATTGCTCAAAG 718

Qy 4150 AATGCCATTTGCTTTTTTGCTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGATTATTA 4209
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  719 AATGCCATTTGCTTTTTTGCTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGATTATTA 778

Qy 4210 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAGAAAAAATTACATTTTTGTTTTTAC 4269
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  779 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAGAAAAAATTACATTTTTGTTTTTAC 838

Qy 4270 CACCTTCAACTAAATTTAATTTATTCCATTGCGAATAGAGCCATAAACTTCAAAGTG 4329
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  839 CACCTTCAACTAAATTTAATTTATTCCATTGCGAATAGAGCCATAAACTTCAAAGTG 898

Qy 4330 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATAGTAT 4389
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  899 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 958

Qy 4390 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAGTGAAATATTATTACTCAAACTACTTTGAAAT 4449
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  959 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAGTGAAATATTATTACTCAAACTACTTTGAAAT 1018

Qy 4450 TAGAACCTCCTGCTGGATCCTGTTGTTTTTAACATAAATAAATACATGTTTAAAATTTTGATA 4509
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1019 TAGAACCTCCTGCTGGATCCTGTTGTTTTTAACATAAATAAATACATGTTTAAAATTTTGATA 1078

Qy 4510 TTTTGATAATCATATTTCATTATCATTTGTTTTCCTTTGTAATCTATATTTTATATATTTG 4569
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1079 TTTTGATAATCATATTTCATTATCATTTGTTTTCCTTTGTAATCTATATTTTATATATTTG 1138

Qy 4570 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCCAATGAGGTTCTTGGCCATGCACAC 4629
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1139 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCCAATGAGGTTCTTGGCCATGCACAC 1198

Qy 4630 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGCCTGAGATGCAAGACT 4689
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1199 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGCCTGAGATGCAAGACT 1258

Qy 4690 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGTGAGGGGGGGAA 4749
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1259 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGTGAGGGGGGGAA 1318

Qy 4750 ATCTGCCGCCTTCTATAGGAATGCTCTCCCTGAGCCTGGTGCGTTCTTGTTGTTC 4809
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1319 ATCTGCCGCCTTCTATAGGAATGCTCTCCCTGAGCCTGGTGCGTTCTTGTTGTTC 1378

Qy 4810 TGGCTGGCTGTGTATTTTTCTGTCCCTGCTACGTCTTAAGGACTTGTTTGGATCTCCA 4869
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1379 TGGCTGGCTGTGTATTTTTCTGTCCCTGCTACGTCTTAAGGACTTGTTTGGATCTCCA 1438

Qy 4870 GTTCCTAGCACATAGTGCCTGGCACAGTTGCAGGTTTGCAGAGTGAATGGAA 4929
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1439 GTTCCTAGCACATAGTGCCTGGCACAGTTGCAGGTTTGCAGAGTGAATGGAA 1498

Qy 4930 ATATAAACTAGAAATAATATCCTTGTTGAAATCAGCACCACCAGTCCTGGTAAGTGT 4989
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1499 ATATAAACTAGAAATAATATCCTTGTTGAAATCAGCACCACCAGTAGTCCTGGTAAGTGT 1558
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;  TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
;  CURRENT APPLICATION NUMBER: US/09/306,828
;  CURRENT FILING DATE: 1999-05-07
;  EARLIER APPLICATION NUMBER: US 09/227,881
;  EARLIER FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: Microsoft Word 97
;  SEQ ID NO 37
;  LENGTH: 283
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-306-828-37

Query Match             4.3%;  Score 227;  DB 3;  Length 283;
Best Local Similarity  100.0%;
Matches  227;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      5045 AACTATTATTGGGGTATGGTGCATAAATTGGATGTTCTTTTTAAAAAGAAACTCCAAA 5104
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 AACTATTATTGGGGTATGGTGCATAAATTGGATGTTCTTTTTAAAAAGAAACTCCAAA 60

Qy      5105 CAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTG 5164
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTG 120

Qy      5165 TGCACAGCCCCACCCAGCCTCACGTGGCCACCTTCTGTCTTCCCCATGAAGGGCTGGCTC 5224
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 TGCACAGCCCCACCCAGCCTCACGTGGCCACCTTCTGTCTTCCCCATGAAGGGCTGGCTC 180

Qy      5225 CCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             |||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 227
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RESULT 13
US-09-949-016-15356/c
;  Sequence 15356, Application US/09949016
;  Patent No. 6812339
;  GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 15356
;  LENGTH: 29326
;  TYPE: DNA
;  ORGANISM: Human
US-09-949-016-15356

Query Match             3.6%;  Score 189.8;  DB 3;  Length 29326;
Best Local Similarity  78.5%;  Pred. No. 7.4e-36;
Matches  227;  Conservative   0;  Mismatches  62;  Indels   0;  Gaps   0;

Qy      1280 AGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCACCTGAGCTCACTGCAACC 1339
             ||  |||  ||||||| ||  ||| | ||||| | || ||||||||||||||||||||
Db     23969 AGAGTCTCACTCATTACCAGGTGAGTGCAGTGCAATTCTCGGCTCATTGCAACC 23910

Qy      1340 TCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCCGGGCGTAGCTGGGACTACAG 1399
             ||||||||||  |||  ||||||||||||||||||| |||| || |||||||||||
Db     23909 TCTGCCTCCCAGGTTCAAGTGATTCATGTTAGCTTCCCGAGTAGCTGGGACTACAG 23850

Qy      1400 GCGCACGCCCGGCTAATTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCG 1459
             ||  |||||| || ||||||||| ||||||||||||||||||||||||||
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Db     23849 GCACACGCCCAGCTAATTTTGTATTTTTAGTACAGATGGGGTTTCGCCGTATTGGCCAG 23790
Qy      1460 GCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAG 1519
             |||||||||||||||||||||||||||||||||||||||||||
Db     23789 GCTGGTCTCAAACTCCTGACCTCAGGTGATCCACCCGCCTCCTAAAGTGCTGGG 23730

Qy      1520 ATTACAGGCATGAGTCACGGCCGCCGGCCGCCAAGGGTCAGTGTTAATAAG 1568
             |||||||||||||||||||| ||||  ||||||||||||||||||| |||||
Db     23729 ATTACAGTGTGAGCCACCGCGCCTGGAAAGGGGTTTTAAAGTAG 23681
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RESULT 14
US-09-949-016-15851/c
;  Sequence 15851, Application US/09949016
;  Patent No. 6812339
;  GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 15851
;  LENGTH: 205044
;  TYPE: DNA
;  ORGANISM: Human
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)...(205044)
;  OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15851

Query Match             3.5%;  Score 184.6;  DB 3;  Length 205044;
Best Local Similarity  78.0%;  Pred. No. 3.6e-34;
Matches  238;  Conservative   0;  Mismatches  59;  Indels   8;  Gaps   1;

Qy      1280 AGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACC 1339
             ||  |||  |||||||||| ||  ||| | ||||| | || ||||||||||||||||||||
Db    161178 AGAGTCTTGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCACCATCTCGGCTCACTGCAACC 161119

Qy      1340 TCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCCGGGCGTAGCTGGGACTACAG 1399
             |||||||||||||||||||||||||||||||||||| |||| || |||||||||||
Db    161118 TCCGCCTCCCGGGTTCAAGCAATTCTCCCGCCTCAGCCTCCCGAGTAGCTGGGACTACAG 161059

Qy      1400 GCG------CACGCCCGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATA 1451
             |||      |||||||||||| |||||||||||||||||||||||||||||||
Db    161058 GCGCCTGCCACCACGCCCGGCTAATTTTTGTATTTTTAGTAGAGACGGGATTTCACCATG 160999

Qy      1452 TTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCCTAAA 1511
             ||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      1512 GTGCTGGGATTACAGGCATGAGTCAGGGTCAGTGTTAATAAGGAA 1571
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Qy      1572 TAACT 1576
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;  Sequence 15852, Application US/09949016
;  Patent No. 6812339
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; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15852
;  LENGTH: 205044
;  TYPE: DNA
;  ORGANISM: Human
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)...(205044)
;  OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15852

Query Match      3.5%;   Score 184.6;  DB 3;  Length 205044;
Best Local Similarity  78.0%;   Pred. No. 3.6e-34;
Matches  238;  Conservative   0;  Mismatches   59;  Indels    8;  Gaps    1;

Qy    1280 AGGGTGAGGGTCTGGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACC 1339
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Db  161178 AGAGTCTTGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCACCATCTCGGCTCACTGCAACC 161119

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Db  161118 TCCGCCTCCCGGGTTCAAGCAATTCTCCCGTCTCAGCCTCCTGAGTAGCTGGGACTACAG 161059

Qy    1400 GCG-------CACGCCCGGCTAATTTTGTATTGTTAGTAGAGATGGGGTTTCACCATA 1451
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Db  161058 GCGCCTGCCACCACGCCCGGCTAATTTTTGTATTTTTAGTAAAGACGGGATTTCACCATG 160999

Qy    1452 TTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAA 1511
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Qy    1512 GTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCCAAGGGTCAGTGTTTAATAAGGAA 1571
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Db  160938 GTGCTGGGATTACAGGCATGAGCCACCCTGCCCTGGCCAAGACGTGATTATTTTTAAGAAT 160879

Qy    1572 TAACT 1576
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Db  160878 AAAAT 160874
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Search completed: January 26, 2006, 04:23:24
Job time : 614 secs

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                    GenCore version 5.1.6
       Copyright  (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   January 26, 2006, 03:55:20 ; Search time 2551 Seconds
                                        (without alignments)
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Title:           US-09-227-881-34
Perfect score:   5271
Sequence:        1 atctttgttcagttacctc.........tcgggcatgagccagcaagg 5271

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters:   19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Published Applications NA Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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	2	5271	100.0	6169	5	US-10-244-633-3	Sequence 3, Appli
	3	5246.4	99.5	5300	5	US-09-985-637A-1	Sequence 1, Appli
	4	5246.4	99.5	5300	5	US-10-244-633-1	Sequence 1, Appli
	5	5246.4	99.5	5300	7	US-10-741-339-1	Sequence 1, Appli
	6	5233.4	99.3	37252	5	US-10-087-192-1228	Sequence 1228, Ap
	7	5224.4	99.1	5304	5	US-10-244-633-2	Sequence 2, Appli
	8	4017.4	76.2	6000	3	US-09-952-464A-1	Sequence 1, Appli
	9	1804.4	34.2	2800	6	US-10-017-870-10	Sequence 10, Appl
c	10	1804.4	34.2	2800	8	US-10-278-698-294	Sequence 294, App
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	12	1804.4	34.2	2800	9	US-10-803-557-10	Sequence 10, Appl
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	19	394.4	7.5	1086	7	US-10-723-860-927	Sequence 927, App
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	25	227	4.3	227	5	US-10-244-633-38	Sequence 38, Appl
	26	227	4.3	227	5	US-10-244-633-37	Sequence 37, Appl
	27	222.6	4.2	30057	8	US-10-087-192-1225	Sequence 1225, Ap
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c	29	189.8	3.6	37443	8	US-10-719-993-6853	Sequence 6853, Ap
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c	33	184.2	3.5	70779	5	US-10-087-192-1012	Sequence 1012, Ap
	34	183.2	3.5	41936	9	US-09-967-768A-116	Sequence 116, App
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c	36	183.2	3.5	104245	7	US-10-160-807-4	Sequence 4, Appli
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	38	183.2	3.5	170245	9	US-10-717-597-322	Sequence 322, App
c	39	182.2	3.5	5367	7	US-10-450-763-16437	Sequence 16437, A
	40	181.2	3.4	196063	6	US-09-925-065A-127303	Sequence 127303,
c	41	181.2	3.4	560	7	US-10-322-281-612	Sequence 612, App
	42	180.6	3.4	1620	6	US-09-925-065A-67041	Sequence 67041, A
	43	180.6	3.4	1620	4	US-09-925-065A-67042	Sequence 67042, A
	44	180.6	3.4	39725	4	US-10-017-161-1611	Sequence 1611, Ap
	45	180.6	3.4	39729	6	US-10-292-798-1285	Sequence 1285, Ap

ALIGNMENTS

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; Sequence 34, Application US/10244633
; Publication No. US20030068640A1
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
; TITLE OF INVENTION:  Prognosis And Treatment Of Glaucoma And Related
; TITLE OF INVENTION:  Disorders
; FILE REFERENCE: 07425.0057.US01
; CURRENT APPLICATION NUMBER: US/10/244,633
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US/09/306,828
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/227,881
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 34
; LENGTH: 5271
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-633-34

  Query Match             100.0%;  Score 5271;  DB 5;  Length 5271;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
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Qy   181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGTAAATC 240
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Qy  1321  ACCTGAGCTCACTGCAACCTCTGCCTCCCAGTTCAAGCAATTCTCCTGTCTCAGCCTCC  1380
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Qy  1381  CGCGTAGCTGGGACTACAGGCGCCACGCCGGCTAATTTTGTATTGTTAGTAGAGATGGG  1440
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Qy  1561  TTAATAGGAATAACTGAATGGTTTACTAAACCAACAGGAAACAGACAAAAGCTGTGA     1620
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Qy  1741  CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG  1800
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Qy  1921  TGGGTGTCCTGAGCAACCTGCCAGCCCGTGTGTTTGTTTTGTTTTGTTATCACTTCTCTAGG  1980
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Qy  2101  CCTACCTTCGTGCGAGGTGACAGTTTCTCATGGAAGAAAATGGTGAAGAAATTAATAGCCA  2160
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Qy  2221  AGCATCCCTTACAAGGCCACTCCCTAGCGCCCCTGCCTCCATCGTGCCCGGAGG      2280
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Qy  2281  CCCCCAAGCCCGAGTCTTCCAAGCGCTGCAGCTGGCTGGGACTCCTTGGCTCCCAGGCT  2340
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Qy  2341  GCTCGCTTCCCGTGAATCGTCCTGTGCATCTGAGCTGGGACTCTGGAGACTCTAC      2400
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Db   241  CATCAAACAGGAGCTAAGAAACAGGAGAATGAGATGGGCACTTGCCCAAGGAAAATGCCAG  300

Qy   301  GAGAGCAAATATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG    360
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Qy   361  ATGAGGACCAAAATCAATGATTAAGGAAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG  420
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Qy   421  TAATTAAGTATTTGTTCCTTGGGAAGAGACCTTCCATGTGAGCTTGATGGAAAATGGGAA  480
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Qy   481  AAACGTCAAAAGCATGATCAGATCCCAAAGTCGATTATTATTTTAAAAACCAGAT     540
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Db   481  AAACGTCAAAAGCATGATCAGATCCCAAAGTCGATTATTATTTTAAAAACCAGAT     540

Qy   541  GGCATCACTCTGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC   600
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Qy   601  AGCAAAATCAAAATTCCGCAACACCTCCGTCTATACCAGGGAACACAAAA           660
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Qy   661  AGTGATTAGGCCAGTGACTTGACCATGTTCGCAACACTGGGAAATGAAAAACTGAGAGACAAAA  720
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Qy   781  GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCTCAGCA  840
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Qy   901  TTGAAAGATCATGAATTTAACCATTTTAAGTATAAACAAATATGCGATGCATAATCAG   960
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Qy  1201  TGTGCAGCCAAGTCTCCGCTCCACAGAAGTCTCCCACTTCTGCATCACGATGT      1260
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3541 GTTCTTAGGAGGCAGGGCTATATGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3541 GTTCTTAGGAGGCAGGGCTATATGTGGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600

Qy 3601 CCTGATTTCTTAATACTATATTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3601 CCTGATTTCTTAATACTATATTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660

Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTCTCCCTTATTAGGAACTCTTTTCTTCTGAGC 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTCTCCCTTATTAGGAACTCTTTTCTTCTGT 3720

Qy 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTCTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTCTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780

Qy 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTCGACTATATGATGATTGGTTTTTGAAAAAT 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTCGACTATATGATGATTGGTTTTTGAAAAAT 3840

Qy 3841 CATTTCAGCGATGTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTGGTCAGCTG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3841 CATTTCAGCGATGTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTGGTCAGCTG 3900

Qy 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGCGGCTTAACTGCAGAACCAATCAAAA 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGCGGCTTAACTGCAGAACCAATCAAAA 3960

Qy 3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCGGAGGTGAGTCTGCCAGGGC 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCGGAGGTGAGTCTGCCAGGGC 4020

Qy 4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080

Qy 4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTCGTGTATAT 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTCGTGTATAT 4140

Qy 4141 TTATTGGCTATTGCCATTTGCTTTTTGCTTTTGTTTTTTGGGTTTATTAATGTAAAGCAG 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4141 TTATTGGCTATTGCCATTTGCTTTTTGCTTTTGTTTTTTGGGTTTATTAATGTAAAGCAG 4200

Qy 4201 GGATTATTAACCTACAGTGTTGCAGATACGTTGTAAGTACGTTGTTGCAGAATATTTACATTTT 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4201 GGATTATTAACCTACAGTGTTGCAGATACGTTGTAAGTACGTTGTTGCAGAAATTTACATTTT 4260

Qy 4261 TGTTTTTACCACCTTCTAACTAAATTTATTCCATTGCGAATAGAGCCATAAA 4320
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4261 TGTTTTTACCACCTTCTAACTAAATTTATTCCATTGCGAATAGAGCCATAAA 4320

Qy 4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTGTCATTACCAATAGAAATCACAGACATT 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTGTCATTACCAATAGAAATCACAGACATT 4380

Qy 4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTATACTCAAAACTA 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTATACTCAAAACTA 4440

Qy 4441 CTTTGAAATTAGACCTCCTGCTGATCTGTTTTTAACATATTAATAAACATGTTTAAA 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4441 CTTTGAAATTAGACCTCCTGCTGATCTGTTTTTAACATATTAATAAACATGTTTAAA 4500

Qy 4501 ATTTTGATATTTTGATAATCATTATTGTTTCCTTTGTAATCTATATTTT 4560
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 4501 ATTTTGATATTTTGATAATCATTATTGTTTCCTTTGTAATCTATATTTT 4560

Qy 4561 ATATATTTGAAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4561 ATATATTTGAAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620

Db 2401 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 2460
          CCAGAAAGGAATGGAGAGGGAACTAGTCTAACGAGAATCTGGAGGGGACAGTGTTTC
Qy 2461 CTCAGAGGGAATGGGCCTTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGGCAGGGAG 2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2461 CTCAGAGGGAATGGGCCTTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGGCAGGGAG 2520

Qy 2521 TGGGGACGCTGGGCTGGGCTGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2521 TGGGGACGCTGGGCTGGGCTGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580

Qy 2581 GCTGCCCAGATGTTCAGTTGTTCACCGGGCTGGGAGTTTCCGTTGCTTCCTGTGAGC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2581 GCTGCCCAGATGTTCAGTTGTTCACCGGGCTGGGAGTTTCCGTTGCTTCCTGTGAGC 2640

Qy 2641 CTTTTATCTTTTCTCTGCTTGGAGGAGAAGCAGCTCTATTTCATGAAGGGATGCAGTTTC 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2641 CTTTTATCTTTTCTCTGCTTGGAGGAGAAGCAGCTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy 2701 ATAAAGTCAGCTGTTAAAATTCAGGGTGTGCATGGGTTTTCTTCCACGAAGGCCTTTAT 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2701 ATAAAGTCAGCTGTTAAAATTCAGGGTGTGCATGGGTTTTCTTCCACGAAGGCCTTTAT 2760

Qy 2761 TTAATGGGAATATAGGAGCGAGCTCATTTCCTAGGCCGTTAATTCCACGGAAGAAGTGAC 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2761 TTAATGGGAATATAGGAGCGAGCTCATTTCCTAGGCCGTTAATTCCACGGAAGAAGTGAC 2820

Qy 2821 TGGAGTCTTTCTTTCCATGCTCTCGTTCTGTGTTCGGGCCAACTACTGGGCTTA 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2821 TGGAGTCTTTCTTTCCATGCTCTCGTTCTGTGTTCGGGCCAACTACTGGGCTTA 2880

Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTCTGGTTCTCGCCATT 2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTCTGGTTCTCGCCATT 2940

Qy 2941 GGTTGGCTGTGCGACCGTGGGGCAAGTCTCTCCTTCCCGGGCCCATAGTCTTCTCTGCT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2941 GGTTGGCTGTGCGACCGTGGGGCAAGTCTCTCCTTCCCGGGCCCATAGTCTTCTCTGCT 3000

Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGGATTCTCTGTGTGAGGGG 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGGATTCTCTGTGTGAGGGG 3060

Qy 3061 GGATGTTGAGAGGGGAAGGAGGAGCAGCAGAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3061 GGATGTTGAGAGGGGAAGGAGGAGCAGCAGAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3120

Qy 3121 GGACAGGAAGGCAGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3121 GGACAGGAAGGCAGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180

Qy 3181 CAGGACCCGAGAGCTTCAGGAAAGCTCAATGAACCCAACAGCCCACATTTTCCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3181 CAGGACCCGAGAGCTTCAGGAAAGCTCAATGAACCCAACAGCCCACATTTTCCT 3240

Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAGAACTAACTGGT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAGAACTAACTGGT 3300

Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCGAGAGATTG 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCGAGAGATTG 3360

Qy 3361 TTAAACTTTTCACCCTGACCTGCTGCTCAGTGACTGCTGACAGCACGG 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db 3361 TTAAACTTTTCACCCTGACCTGCTGCTCAGTGACTGCTGACAGCACGG 3420

Qy 3421 AGTGACCTGCAGCGCGCGCAGGGAGAGAAAAAGAGGGGATAGTGTATGAGCAAGAAAAG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3421 AGTGACCTGCAGCGCGCGCAGGGAGAGAAAAAGAGGGGATAGTGTATGAGCAAGAAAAG 3480

Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCCACCAGGGATTATAGTCCACGTGATCCTGG 3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Query Match       100.0%;  Score 5271;  DB 5;  Length 6169;
Best Local Similarity 100.0%;  Pred. No. 0;  Indels 0;  Gaps 0;
Matches 5271;  Conservative 0;  Mismatches 0;

Qy     1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG    60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG    60

Qy    61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA   120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA   120

Qy   121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAAGTGTCCAAGTGTCTTATTTTAGTGA   180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAAGTGTCCAAGTGTCTTATTTTAGTGA   180

Qy   181 CAGATGTTGCTCCTGACAGAGCTATTCTTCAGGAAACATCACATCCAATGTGTAAATC    240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CAGATGTTGCTCCTGACAGAGCTATTCTTCAGGAAACATCACATCCAATGTGTAAATC    240

Qy   241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGCACTTGCCCAAGGAAAAATGCCAG   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGCACTTGCCCAAGGAAAAATGCCAG   300

Qy   301 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTGTTTTTTAATTTCAGGAAAAATG   360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTGTTTTTTAATTTCAGGAAAAATG   360

Qy   361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAGATGTTTCCAAATTGG   420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAGATGTTTCCAAATTGG   420

Qy   421 TAATTAAGTAGTATTGTTCCTTGGGAGGACATGATCAGATCCAAAGTGGATGGAAATGGAA   480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TAATTAAGTAGTATTGTTCCTTGGGAGGACATGATCAGATCCAAAGTGGATGGAAATGGAA   480

Qy   481 AAACGTCAAAAGCATGATCAGATCCAAAGTGGATCATGTTAGCAAAGGACATAACAATAAC   540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AAACGTCAAAAGCATGATCAGATCCAAAGTGGATCATGTTAGCAAAGGACATAACAATAAC   540

Qy   541 GGCATCACTCTGGGAGGCAAGTCAGGAAGTCATGTGGGACTGGGAAAATGGGGACTGGGAA   600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGCATCACTCTGGGAGGCAAGTCAGGAAGTCATGTGGGACTGGGAAAATGGGGACTGGGAA   600

Qy   601 AGCAAAATCAAAATTCCGACAAATCAGGAGGAAAATGGGGACTGGGAAAAGCTTTCATAAC   660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AGCAAAATCAAAATTCCGACAAATCAGGAGGAAAATGGGGACTGGGAAAAGCTTTCATAAC   660

Qy   661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCGTCATACCAGGGAACACAGAACAAA   720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCGTCATACCAGGGAACACAGAACAAA   720

Qy   721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA   780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA   780

Qy   781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAAGCAGTGCCCCTCAGCA   840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAAGCAGTGCCCCTCAGCA   840

Qy   841 GGGACCCTGAGGCATTGCCTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC   900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GGGACCCTGAGGCATTGCCTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC   900

Qy   901 TTGAAAGATCATGAATTTTAAGTATAAAACAAATATGCATAATATCAG   960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TTGAAAGATCATGAATTTTAAGTATAAAACAAATATGCATAATATCAG   960

Qy  1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCATCTGTCCCAACTTTTTCAGAATGATC  1080
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Qy  4621 CATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA  4680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4621 CATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA  4680

Qy  4681 TGCAAGACTGAAATTAGAAAGTCTCCAAAGATACACAGTTGTTTTAAAGCTTAGGGGTG  4740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4681 TGCAAGACTGAAATTAGAAAGTCTCCAAAGATACACAGTTGTTTTAAAGCTTAGGGGTG  4740

Qy  4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC  4800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC·  4800

Qy  4801 CTTGTGTTCTGGCTGGCTGTATTTTCTCTGTCCCCTGCTACGTCTTAAAGGACTTGTTT  4860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4801 CTTGTGTTCTGGCTGGCTGTATTTTCTCTGTCCCCTGCTACGTCTTAAAGGACTTGTTT  4860

Qy  4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACGAGTTCTCAATGAGTTTGCAGAG  4920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACGAGTTCTCAATGAGTTTGCAGAG  4920

Qy  4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGTGAAAATCAGCACCACCAGTAGTCCTGG  4980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGTGAAAATCAGCACCACCAGTAGTCCTGG  4980

Qy  4981 TGTAAGTGTGTACGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGAGATA  5040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4981 TGTAAGTGTGTACGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGAGATA  5040

Qy  5041 TAGGAACTATTATTGGGTATGGGTGCATAAATTGGATGTTCTTTTTAAAAGAAACTC  5100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5041 TAGGAACTATTATTGGGTATGGGTGCATAAATTGGATGTTCTTTTTAAAAGAAACTC  5100

Qy  5101 CAAAACAGAGACTTCTGGAAGGTTATTTTCTAAGAAATCTTGCTGCGTGGCAGGCAACCCC  5160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5101 CAAAACAGAGACTTCTGGAAGGTTATTTTCTAAGAAATCTTGCTGCGTGGCAGGCAACCCC  5160

Qy  5161 CCTGTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCATGAAGGGCTG  5220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5161 CCTGTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCATGAAGGGCTG  5220

Qy  5221 GCTCCCCAGTATATATAAAACCTTCTCTGGAGCTCGGGCATGAGCCAGCAAGG  5271
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Db  5221 GCTCCCCAGTATATATAAAACCTTCTCTGGAGCTCGGGCATGAGCCAGCAAGG  5271
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RESULT 2
US-10-244-633-3
; Sequence 3, Application US/10244633
; Publication No. US2003006840A1
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 07425.0057.US01
; CURRENT APPLICATION NUMBER: US/10/244,633
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US/09/306,828
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/227,881
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
;
; SEQ ID NO 3
; LENGTH: 6169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-633-3

This page contains a dense DNA/nucleotide sequence alignment between two sequences labeled **Db** and **Qy**, arranged in two blocks of rows across the page. Each row is labeled with the start position number, the nucleotide sequence, and the end position number.

Left block (positions 1021–2160):

Label	Start	End
Db	1021	1080
Qy	1081	1140
Db	1081	1140
Qy	1141	1200
Db	1141	1200
Qy	1201	1260
Db	1201	1260
Qy	1261	1320
Db	1261	1320
Qy	1321	1380
Db	1321	1380
Qy	1381	1440
Db	1381	1440
Qy	1441	1500
Db	1441	1500
Qy	1501	1560
Db	1501	1560
Qy	1561	1620
Db	1561	1620
Qy	1621	1680
Db	1621	1680
Qy	1681	1740
Db	1681	1740
Qy	1741	1800
Db	1741	1800
Qy	1801	1860
Db	1801	1860
Qy	1861	1920
Db	1861	1920
Qy	1921	1980
Db	1921	1980
Qy	1981	2040
Db	1981	2040
Qy	2041	2100
Db	2041	2100
Qy	2101	2160

Right block (positions 2101–3240):

Label	Start	End
Db	2101	2160
Qy	2161	2220
Db	2161	2220
Qy	2221	2280
Db	2221	2280
Qy	2281	2340
Db	2281	2340
Qy	2341	2400
Db	2341	2400
Qy	2401	2460
Db	2401	2460
Qy	2461	2520
Db	2461	2520
Qy	2521	2580
Db	2521	2580
Qy	2581	2640
Db	2581	2640
Qy	2641	2700
Db	2641	2700
Qy	2701	2760
Db	2701	2760
Qy	2761	2820
Db	2761	2820
Qy	2821	2880
Db	2821	2880
Qy	2881	2940
Db	2881	2940
Qy	2941	3000
Db	2941	3000
Qy	3001	3060
Db	3001	3060
Qy	3061	3120
Db	3061	3120
Qy	3121	3180
Db	3121	3180
Qy	3181	3240
Db	3181	3240

RESULT 3
US-09-985-637A-1
; Sequence 1, Application US/09985637A
; Publication No. US20030119000A1
; GENERAL INFORMATION:
; APPLICANT: Polansky, Jon
; TITLE OF INVENTION: METHODS TO SCREEN AND TREAT INDIVIDUALS WITH GLAUCOMA OR THE P!
; TITLE OF INVENTION: TO DEVELOP GLAUCOMA

```
;  FILE REFERENCE: 13587.296
;  CURRENT APPLICATION NUMBER: US/09/985,637A
;  CURRENT FILING DATE: 2001-11-05
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;  LENGTH: 5300
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-985-637A-1

Query Match      99.5%;   Score 5246.4;   DB 3;   Length 5300;
Best Local Similarity   99.9%;   Pred. No. 0;
Matches 5269;   Conservative   0;   Mismatches   0;   Indels   2;   Gaps   2;
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Qy      1  ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG   60

Qy     61  TCCTATAAACTGTATAGCCTCCATTCGATGTATGTCTTTGCAGGATGATAAAGAATCA   120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  TCCTATAAACTGTATAGCCTCCATTCGATGTATGTCTTTGCAGGATGATAAAGAATCA   120

Qy    121  GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTTATTTTAGTGA   180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTTATTTTAGTGA   180

Qy    181  CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAAACATCATCCAATATGGTAAATC   240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAAACATCATCCAATATGGTAAATC   240

Qy    241  CATCAAACAGGAGCTAAGAACAGAGATGAGAAACAGGAGATGAGGAAAAATGCCAG   300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  CATCAAACAGGAGCTAAGAACAGAGATGAGAAACAGGAGATGAGGAAAAATGCCAG   300

Qy    301  GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTAATTCAGGAAAAATG   360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTAATTCAGGAAAAATG   360

Qy    361  ATGAGGACCAAAATCAATGAATAAGGAAAAACAGCTCAGAAAAAAGTGTTTCCAARTTGG   420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  ATGAGGACCAAAATCAATGAATAAGGAAAAACAGCTCAGAAAAAAGTGTTTCCAAATTGG   420

Qy    421  TAATTAAGTATTTGTTCCTTGGAAGAGACCTTCCATGTGAGCTTGATGGAAAATGGGAA   480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  TAATTAAGTATTTGTTCCTTGGAAGAGACCTTCCATGTGAGCTTGATGGAAAATGGGAA   480

Qy    481  AAACGTTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT   540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  AAACGTTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT   540

Qy    541  GGCATCACTCTGGGGAGGCAAGTTCAGGAAGTCATGTTAGCAAAGACATAACAATAAC   600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GGCATCACTCTGGGGAGGCAAGTTCAGGAAGTCATGTTAGCAAAGACATAACAATAAC   600

Qy    601  AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAAATGGGGACTGGGAAAGCTTTCATAAC   660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAAATGGGGACTGGGAAAGCTTTCATAAC   660

Qy    661  AGTGATTAGGCAGTTGACCATGTTCGCCAACACCTCCGTCTATACCAGGGAACACAAAA   720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  AGTGATTAGGCAGTTGACCATGTTCGCCAACACCTCCGTCTATACCAGGGAACACAAAA   720

Qy    721  ATTGACTGGCTAAGCCTGGACTTTCAAGGCCTTCAAGGGAAAATGAAAAACTGAGAGCAAAACAAAA   780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  ATTGACTGGCTAAGCCTGGACTTTCAAGGCCTTCAAGGGAAAATGAAAAACTGAGAGCAAAACAAAA   780

Qy    781  GACATGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA   840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GACATGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA   840

Qy    841  GGGACCCTGAGGCATTGCCTTGGAAGGCCAGTTTTCTTAGGAATCTTAAGAAACTC   900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  GGGACCCTGAGGCATTGCCTTGGAAGGCCAGTTTTCTTAGGAATCTTAAGAAACTC   900

Qy    901  TTGAAAGATCATGAATTTAACCATTTTAAGTATAAAACAAATATGCGATCATAATCAG   960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATCATAATCAG   960

Qy    961  TTTAGACATGGGTCCCAATTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC   1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TTTAGACATGGGTCCCAATTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC   1020

Qy   1021  GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC   1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC   1080

Qy   1081  TGTCATAGCCCTCACCACACAGGCCCGATGTGTCTGACCTACCAACCACATCTACAACCCAA   1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  TGTCATAGCCCTCACCACACAGGCCCGATGTGTCTGACCTACCAACCACATCTACAACCCAA   1140

Qy   1141  GTGCCTCAACCATTGTAAGCTGTCATCTCAGTAGGTCCATTCAGTTCCACCTCCCC   1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  GTGCCTCAACCATTGTAAGCTGTCATCTCAGTAGGTCCATTCAGTTCCACCTCCCC   1200

Qy   1201  TGTGCAGCCCATCCGCTCCACAGGAAGTCTCCCCACTCAGACTTCTGCATCACGATGT   1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  TGTGCAGCCCATCCGCTCCACAGGAAGTCTCCCCACTCAGACTTCTGCATCACGATGT   1260

Qy   1261  TACAGCCAGAAGCTCCGTGAGGGTGAGGGTTCGTGTCTTACACCTGTATGCTCTAC   1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  TACAGCCAGAAGCTCCGTGAGGGTGAGGGTTCGTGTCTTACACCTGTATGCTCTAC   1320

Qy   1321  ACCTGAGCTCACTGCAACCTCTGCCTCCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTC   1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  ACCTGAGCTCACTGCAACCTCTGCCTCCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTC   1380

Qy   1381  CGCGTAGTCTGGGACTACAGGCGCACGCCGGCTAATTTTGTATTGTTAGTAGTAGATGGG   1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CGCGTAGTCTGGGACTACAGGCGCACGCCGGCTAATTTTGTATTGTTAGTAGTAGATGGG   1440

Qy   1441  GTTTCACCCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC   1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  GTTTCACCCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC   1500

Qy   1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCCCGCCGGCCAAGGGTCAGTGT   1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCCCGCCGGCCAAGGGTCAGTGT   1560

Qy   1561  TTAATAAGGAATAACTTGAAATGGTTTTACTAAACCAACAGGAAACAGACAAAAGCTGTGA   1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  TTAATAAGGAATAACTTGAAATGGTTTTACTAAACCAACAGGAAACAGACAAAAGCTGTGA   1620

Qy   1621  TAATTTCAGGGATTCTTGGGATGGGAATGGCCATGAGCTGCCTGCCTAGTCCCAGAC   1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  TAATTTCAGGGATTCTTGGGATGGGAATGGCCATGAGCTGCCTGCCTAGTCCCAGAC   1680

Qy   1681  CACTGGTCCTCATCACTTTCTCCCTATCCTCATTTTCAGGCTAAGTTACCATTTTATT   1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  CACTGGTCCTCATCACTTTCTCCCTATCCTCATTTTCAGGCTAAGTTACCATTTTATT   1740

Qy   1741  CACCATGCTTTTGTGTAAGCCTCCACATCGTACTGAAATAAGAGTATACATAAACTAG   1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  CACCATGCTTTTGTGTAAGCCTCCACATCGTACTGAAATAAGAGTATACATAAACTAG   1800

Qy   1801  TTCCATTTGGGGGCCATCGTGTGTGTATAGGGGAGGGGGCATACCCCAGAGACTTCCT   1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  TTCCATTTGGGGGCCATCGTGTGTGTATAGGGGAGGGGGCATACCCCAGAGACTTCCT   1860

Qy   1861  TGAAGCCCCGCAGAGGTTCCTCTCCAGCTGGGGGTCCCAAGCACCCGGGTCC   1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  TGAAGCCCCGCAGAGGTTTCCTCTCCAGCTGGGGGGAGCCCGCGGGTCC   1920

Qy   1921  TGGGGTGCTCCTGAGCAACCTGCCAGCCCGTGTCCACTGGTTGTTTGTTGTTATCACTCTCTAGG   1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  TGGGGTGCTCCTGAGCAACCTGCCAGCCCGTGTCCACTGGTTGTTTGTTGTTATCACTCTCTAGG   1980
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Qy   1981 GACCTGTTGCTTTCTATTCTGTGTGACTCGTTCATTCATTGACAATT 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 GACCTGTTGCTTTCTATTCTGTGTGACTCGTTCATTCATTGACAATT 2040

Qy   2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGTGAGCAAAGCAGTCACTGC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGTGAGCAAAGCAGTCACTGC 2100

Qy   2101 CCTACCTTCGTTGGAGTGACAGTTTCTCATGGAAGACGTGCAGAGAAAATTAATAGCCA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCTACCTTCGTTGGAGTGACAGTTTCTCATGGAAGACGTGCAGAGAAAATTAATAGCCA 2160

Qy   2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy   2221 AGCATCCCTTAACAAGCCACCTCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 AGCATCCCTTAACAAGCCACCTCCCTGCTGCCTCCATCGTGCCCGGAGG 2280

Qy   2281 CCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCTCCATCAGTCACAGCCGCTGCAGCTGCCCT 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCTCCATCAGTCACAGCCGCTGCAGCTGCCCT 2340

Qy   2341 GCCTCGCTTCCCGTGAATCGTCCGTGTGACTCGAGCTGGAGTGGAGACTCCTTGGCTCCAGGCT 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 GCCTCGCTTCCCGTGAATCGTCCGTGTGACTCGAGCTGGAGTGGAGACTCCTTGGCTCCAGGCT 2400

Qy   2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGAGGGGACAGTGTTTC 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGAGGGGACAGTGTTTC 2460

Qy   2461 CTCAGAGGGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGCAGGGAG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CTCAGAGGGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGCAGGGAG 2520

Qy   2521 TGGGGACACGCTGAGCCGGGTCTGAGCGGGTGCTGAGAGGGCAGGAAGGTGAAAGC 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TGGGGACACGCTGAGCCGGGTCTGAGCGGGTGCTGAGAGGGCAGGAAGGTGAAAGC 2580

Qy   2581 GCTGCCCAGATGTTCAGTGTGTTCACGGGCTGGGAGTTTCCGTTGCTTCCGTGTGAGC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 GCTGCCCAGATGTTCAGTGTGTTCACGGGCTGGGAGTTTCCGTTGCTTCCGTGTGAGC 2640

Qy   2641 CTTTTATCTTTTCTCTGCTTGCTTCTATTTCATGAGGGATGCAGTTTC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 CTTTTATCTTTTCTCTGCTTGCTTCTATTTCATGAGGGATGCAGTTTC 2700

Qy   2701 ATAAAGTCAGCTGTGTTAAAATTCCAGGGTGTGCATGGGTTTCCTTCACGAAGGCCTTTAT 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 ATAAAGTCAGCTGTGTTAAAATTCCAGGGTGTGCATGGGTTTCCTTCACGAAGGCCTTTAT 2760

Qy   2761 TTAATGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACAGGAAGAAGTGAC 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TTAATGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACAGGAAGAAGTGAC 2820

Qy   2821 TGCAAGACGGTCGAAAACCTTGGAATCAGAGACTCGGTTTCTTCTTGGTTCTCCATT 2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TGCAAGACGGTCGAAAACCTTGGAATCAGAGACTCGGTTTCTTCTTGGTTCTCCATT 2880

Qy   2881 GGTTGGCGTGTGCGACCCGTGGGCAAGTCGGGCCATAGTCTTCTCTGCT 2940
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GGTTGGCGTGTGCGACCCGTGGGCAAGTCGGGCCATAGTCTTCTCTGCT 2940

Qy   2941 ATAAAGACCCCTTGCAGCTTCCGTGTTCTGTGAACACTTCCCGTGATTCTGTGAGGGG 3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 ATAAAGACCCCTTGCAGCTTCCGTGTTCTGTGAACACTTCCCGTGATTCTGTGAGGGG 3000
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Qy   3061 GGATGTTGAGAGGGAAGGAGGAGGCAGAGCTGAGCAGCTGAGCCACAGGGGGAGGTGAGGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 GGATGTTGAGAGGGAAGGAGGAGGCAGAGCTGAGCAGCTGAGCCACAGGGGGAGGTGAGGG 3120

Qy   3121 GGACAGGAAGGCAGGCAGAGCTGGGTGCTCCTCCACTGATCAGTCAGACTC 3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGACAGGAAGGCAGGCAGAGCTGGGTGCTCCTCCACTGATCAGTCAGACTC 3180

Qy   3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGTCAATGAACCCAACAGCCACATTTTCCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGTCAATGAACCCAACAGCCACATTTTCCT 3240

Qy   3241 TCCCTAAGCATAGACAATGGCATTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TCCCTAAGCATAGACAATGGCATTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300

Qy   3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360

Qy   3361 TTAAACTTTCACCCTGACCAGCACCCCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TTAAACTTTCACCCTGACCAGCACCCCAGCTCAGCAGTGACTGCTGACAGCACGG 3420

Qy   3421 AGTGACCTGCAGCGCAGGGAGGAGAAAAGAGAGGGATAGTAGTGTATGAGCAAGAAAG 3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGTGACCTGCAGCGCAGGGAGGAGAAAAGAGAGGGATAGTAGTGTATGAGCAAGAAAG 3480

Qy   3481 ACAGATTCATTCAAGGCAGTGGGAATTGACCACAGGGATTATAGTCCAGTGATCCTGG 3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 ACAGATTCATTCAAGGCAGTGGGAATTGACCACAGGGATTATAGTCCAGTGATCCTGG 3540

Qy   3541 GTTCTAGGAGGCAGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 GTTCTAGGAGGCAGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600

Qy   3601 CCTGATTTCTAATACTATATTTCCTTACAAGCTGAGTAATTCTGAGTAATTCTCTGTCTG 3660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 CCTGATTTCTAATACTATATTTCCTTACAAGCTGAGTAATTCTGAGTAATTCTCACAAG 3660

Qy   3661 GTAGTAACTGAGGCTGTGAAGATTACTTACTTAGTTTCTCCTTATTAGGAACTCCTAGAG 3720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GTAGTAACTGAGGCTGTGAAGATTACTTACTTAGTTTCTCCTTATTAGGAACTCCTAGAG 3720

Qy   3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780

Qy   3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGGTTTTTGAAAAT 3840
          |||||||||||||||||||||||||||||||||||||||||||
Db   3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGGTTTTTGAAAAT 3840

Qy   3841 CATTTCAGCGATGGTGTTACTATCTGATTCAGAAAATGAGAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 CATTTCAGCGATGGTGTTACTATCTGATTCAGAAAATGAGAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

Qy   3901 TAAACAAACACCCAGTTGTAAATGTCTGTAAATGTCTGCAGACCAATCAA- 3959
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 TAAACAAACACCCAGTTGTAAATGTCTGTAAATGTCTGCAGACCAATCAAT 3960

Qy   3960 AAGAATAGAATCTTAGAGCAAACTGTTTTCCACATCTGAGGTGAGTCTGCCAGCGG 4019
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 AAGAATAGAATCTTAGAGCAAACTGTTTTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019

Qy   4020 CAGTTTGGAAATATTTACTTCACAAGTATTGGTATTAACAACATAAAG 4079
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   4020 CAGTTTGGAAATATTTACTTCACAAGTATTGGTATTAACAACATAAAG 4079

Qy   4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTGGTATA 4139
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTGGTATA 4139

Qy   4140 TTTATTGCTATTGCCATTGCTTTGCTTTTGTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4140 TTTATTGCTATTGCCATTGCTTTGCTTTTGTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
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Db   5220 GGCTCCCCAGTATATATAAACCTCTGGGCATGAGCCAGCAAGG 5271

RESULT 4
US-10-244-633-1
; Sequence 1, Application US/10244633
; Publication No. US20030068640A1
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 07425.0057.US01
; CURRENT APPLICATION NUMBER: US/10/244,633
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US/09/306,828
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/227,881
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 1
; LENGTH: 5300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-633-1

Query Match   99.5%; Score 5246.4; DB 5; Length 5300;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 5269; Conservative   0; Mismatches   0; Indels   2; Gaps   2;

Qy   1 ATCTTTGTTCAGTTTACCTCAGGCTATTATGAAGTGCTATTCGGATGAGATAACCAATGTGAAAG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATCTTTGTTCAGTTTACCTCAGGCTATTATGAAGTGCTATTCGGATGAGATAACCAATGTGAAAG 60

Qy   61 TCCTATAAACTGTATAGCCTCCATTCGGATGTCTTGGCAGGATGATGATAAAGAATCA 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCCTATAAACTGTATAGCCTCCATTCGGATGTCTTGGCAGGATGATGATAAAGAATCA 120

Qy   121 GGAAGAAGGAGTATCCAGTTAGCCAAGTGTCCAAGGCTGTGTCTGCTCTTATTTTAGTGA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAAGAAGGAGTATCCAGTTAGCCAAGTGTCCAAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy   181 CAGATGTTGCTCCTGACAGAAGAAGCTATTCTTCAGGAAACATCACATCCAATATGTAAATC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CAGATGTTGCTCCTGACAGAAGAAGCTATTCTTCAGGAAACATCACATCCAATATGTAAATC 240

Qy   241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGAGATGGCACTTGCCCAAGGAAAATGCCAG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGAGATGGCACTTGCCCAAGGAAAATGCCAG 300

Qy   301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTAATTTCAGGAAAAATG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTAATTTCAGGAAAAAATG 360

Qy   361 ATGAGGACCAAAATCAATGAATAGGAAAACAGCTCAGAAAAAAGATGTTCCAAATTGG 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAGGACCAAAATCAATGAATAGGAAAACAGCTCAGAAAAAAGATGTTCCAAATTGG 420

Qy   421 TAATTAAGTATTTGTTCCTTGGGAAGAGACTTCCATGTGAGCTTGATGGGAAATGGGAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TAATTAAGTATTTGTTCCTTGGGAAGAGACTTCCATGTGAGCTTGATGGGAAATGGGAA 480

Qy   481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGATTATTATTTTAAAACCAGAT 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGATTATTATTTTAAAACCAGAT 540

Qy   541 GGCATCACTCTGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGCATCACTCTGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Db 4140 TTTATTGGCTATTGCCATTGCTTTTTGTTTTCTCTTGGGTTTATTAATGTAAAGCA 4199
Qy 4200 GGGATTATTAAACCTACAGTCCCAGAAAGCCTGTGAATTTGAAGGAGGAAAAAATTACATTT 4259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4200 GGGATTATTAAACCTACAGTCCCAGAAAGCCTGTGAATTTGAAGGAGGAAAAAATTACATTT 4259
Qy 4260 TTGTTTTTTACCACCTTCTCAACTAAATTTATTCCATTGCGAATAGAGCCATAA 4319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4260 TTGTTTTTTACCACCTTCTCAACTAAATTTATTCCATTGCGAATAGAGCCATAA 4319
Qy 4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Qy 4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Qy 4440 ACTTTGAAATTAGACCTTCTGGATCTTGTTTTTAACATAATTAATAAAACATGTTTAA 4499
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4440 ACTTTGAAATTAGACCTTCTGGATCTTGTTTTTAACATAATTAATAAAACATGTTTAA 4499
Qy 4500 AATTTTGATATTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4500 AATTTTGATATTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Qy 4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
Qy 4620 GCATGCACACACAGCAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGGCCTGAG 4679
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4620 GCATGCACACACAGCAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGGCCTGAG 4679
Qy 4680 ATGCAAGACTGAAATTAGGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGGT 4739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4680 ATGCAAGACTGAAATTAGGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGGT 4739
Qy 4740 GAGGGGGAAATCGCCGCTTCTATAGGAATGTCTCCCTGGTGTGTGCTGT 4799
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 4740 GAGGGGGAAATCGCCGCTTCTATAGGAATGTCTCCCTGGTGTGTGCTGT 4799
Qy 4800 CCTTGTCTTCTCGGCTGGCTGTGTTATTTTCTCTGTCCCTCCTCTCCCTGTCTTAAAAGGACTTGTT 4859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4800 CCTTGTCTTCTCGGCTGGCTGTGTTATTTTCTCTGTCCCTCCTCTCCCTGTCTTAAAAGGACTTGTT 4859
Qy 4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTGCGA 4919
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTGCGA 4919
Qy 4920 GTGAATGAAATAAAACTAGAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4920 GTGAATGAAATAAAACTAGAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
Qy 4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
Qy 5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTAAAAGAAACT 5099
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTAAAAGAAACT 5099
Qy 5100 CCAAACAGACTTCGGAAGGTTATTTTCTCAAGAATCTTGCTGCTGGCCACCTCTGTTCTTCCCCATCTTGG 5159
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5100 CCAAACAGACTTCGGAAGGTTATTTTCTCAAGAATCTTGCTGCTGGCCACCTCTGTTCTTCCCCATCTTGG 5159
Qy 5160 CCCTGTGCACAGCCCCACCCACGTGGCCACCTCACGTGGCCACCTCTTCTCCCCATGAAGGGCT 5219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5160 CCCTGTGCACAGCCCCACCCACGTGGCCACCTCACGTGGCCACCTCTTCTCCCCATGAAGGGCT 5219
Qy 5220 GGCTCCCCAGTATATATAAACCTCTGGGCATGAGCCAGCAAGG 5271
          |||||||||||||||||||||||||||||||||||||||||||
Db 5220 GGCTCCCCAGTATATATAAACCTCTGGGCATGAGCCAGCAAGG 5271

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Qy   601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAATGGGACTGGGAAAGCTTCATAAC  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAATGGGACTGGGAAAGCTTCATAAC  660

Qy   661 AGTGATTAGGCAGTTGACCATGTTCGCAACACTCCCGTCTATACAGGGAACACAAAA  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGTGATTAGGCAGTTGACCATGTTCGCAACACTCCCGTCTATACAGGGAACACAAAA  720

Qy   721 ATTGACTGGCTAAGCCTGGACTTTCAAGGGAAATATGAGAGACAAAACAAAA      780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAGAGACAAAACAAAA     780

Qy   781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCCTTCAGCA        840
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCAGCAGTGCCCTTCAGCA      840

Qy   841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC  900

Qy   901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATAATGCGATGCATAATCAG  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATAATGCGATGCATAATCAG  960

Qy   961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy  1021 GGATAGGTCAGAAATCATTAGAAATCACTGTCCCCATCCTAACTTTTCAGAAATGATC 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGATAGGTCAGAAATCATTAGAAATCACTGTCCCCATCCTAACTTTTCAGAAATGATC 1080

Qy  1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy  1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCATCACAAATGCCACCTCCCCC 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCCC 1200

Qy  1201 TGTGCAGCCAGCCCATCCCGGCTCTCCGACTTCTCCACTCTAGACTTCTGCGATCACGATGT 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 TGTGCAGCCAGCCCATCCCGGCTCTCCGACTTCTCCACTCTAGACTTCTGCGATCACGATGT 1260

Qy  1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy  1321 ACCTGAGCTCACTGGACTCGACGCGCCACGCGCCCGGCTAATTTTGTATTGTTAGTAGAGATGGG 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 ACCTGAGCTCACTGGACTCGACGCGCCACGCGCCCGGCTAATTTTGTATTGTTAGTAGAGATGGG 1380

Qy  1381 CGGGTAGCTGGGACTACAGGCGCCCGGCCACGCGCCCGGCTAATTTTGTATTGTTAGTAGAGATGGG 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CGGGTAGCTGGGACTACAGGCGCCCGGCCACGCGCCCGGCTAATTTTGTATTGTTAGTAGAGATGGG 1440

Qy  1441 GTTTCACCATGTTAGCCCAGGCTGGTCTTGAACTCCTGACCTCAGGGTCACCACCCCACCTC 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 GTTTCACCATGTTAGCCCAGGCTGGTCTTGAACTCCTGACCTCAGGGTCACCACCCCACCTC 1500

Qy  1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCAACAACAGGGAAAACAGACAAAAGTCGTGA 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCAACAACAGGGAAAACAGACAAAAGTCGTGT 1560

Qy  1561 TTAATAAGGAATAACTTGAATGTTTACTAAACCAACAGGGAAAACAGACAAAAGTCGTGA 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 TTAATAAGGAATAACTTGAATGTTTACTAAACCAACAGGGAAAACAGACAAAAGTCGTGT 1620

Qy  1621 TAATTTCAGGGGATTCTTGGGATGGGGGAATGGTGCCATGAGTCGCCTGCCTCCCAGAC 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 TAATTTCAGGGGATTCTTGGGATGGGGGAATGGTGCCATGAGTCGCCTGCCTCCCAGAC 1680
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Qy  1681 CACTGGTGCCTCATCACTTCTTCCCTCATCCTCATTTCATTTCAGGCTAAGCTTACCATTTATT 1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 CACTGGTGCCTCATCACTTCTTCCCTCATCCTCATTTCATTTCAGGCTAAGCTTACCATTTATT 1740

Qy  1741 CACCATGCTTTTGTGTGAAGCCTCCACATCGTTACTGACATAAGAGTATACATAAACTAG 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 CACCATGCTTTTGTGTGGTAAGCCTCCACATCGTTACTGACATAAGAGTATACATAAACTAG 1800

Qy  1801 TTCCATTTGGGGCCATCTGTGTGTCACATAGGGAGGAGGGGCATACCCCAGAGACTCCT 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 TTCCATTTGGGGCCATCTGTGTGTCACATAGGGAGGAGGGGCATACCCCAGAGACTCCT 1860

Qy  1861 TGAAGCCCCGCAGAGGTTTCCTCTCCAGCTGGGGAGCCCCTGCAAGCACCCGGGTCC 1920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 TGAAGCCCCGCAGAGGTTTCCTCTCCAGCTGGGGAGCCCCTGCAAGCACCCGGGGTCC 1920

Qy  1921 TGGGGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTGTTTGTTTGTTATCACTCTCTAGG 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTGTTTGTTTGTTATCACTCTCTAGG 1980

Qy  1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy  2041 TATTGAGTACTTATATCTGCCAAGACACCAGACACCAGGTGAGCAAAATGGTCACTGC 2100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 TATTGAGTACTTATATCTGCCAAGACACCAGACACCAGGTGAGCAAAATGGTCACTGC 2100

Qy  2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGAGACGTGCGAGAAGAAAATTAATAGCCA 2160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGAGACGTGCGAGAAGAAAATTAATAGCCA 2160

Qy  2161 GCCAACTTAAACCCAGTGCTGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCCAACTTAAACCCAGTGCTGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy  2221 AGCATCCCTTAACAAGGCCACCTCCCTGCTCCCTGCTCCATCGTGCCCGGAGG 2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 AGCATCCCTTAACAAGGCCACCTCCCTGCTCCCTGCTCCATCGTGCCCGGAGG 2280

Qy  2281 CCCCAAGCCCGAGTCTTCCAAGCTCCTCCCTCCCATCAGTCGGCTGCAGCTGGCCT 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 CCCCAAGCCCGAGTCTTCCAAGCTCCTCCCTCCCATCAGTCGGCTGCAGCTGGCCT 2340

Qy  2341 GCTCGCTTCCCGTGAATCGTCGTGGTGCATCGCTGGAGGAGACTCCTGGCTCCAGGCT 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 GCCTCGCTTCCCGTGAATCGTCGTGGTGCATCGCTGGAGGAGACTCCTGGCTCCAGGCT 2400

Qy  2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGGGAATCTGGAGGGGGACAGTGTTTC 2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGGGAATCTGGAGGGGGACAGTGTTTC 2460

Qy  2461 CTCAGAGGGAAAGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGACTCGAGGGAG 2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CTCAGAGGGAAAGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGACTCGAGGGAG 2520

Qy  2521 TGGGGACCTGGGGCTGAGCGGTGCTGAAAAGGCCAGGAAGGTGAAAGGCTGAA 2580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 TGGGGACCTGGGGCTGAGCGGTGCTGAAAAGGCCAGGAAGGTGAAAGGCTGAA 2580

Qy  2581 GCTGCCCAGATGTTCAGTGTGTTCAGGGGCTTTCCGTTCCTTCCTGTGAGC 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 GCTGCCCAGATGTTCAGTGTGTTCAGGGGCTTTCCGTTCCTTCCTGTGAGC 2640

Qy  2641 CTTTTATTCTTTTCTCTGCTTCTCATGAAGGGATGCTATTTCATTGAAGGGATGCGAGTTTC 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 CTTTTATTCTTTTCTCTGCTTCTCATGAAGGGATGCTATTTCATTGAAGGGATGCGAGTTTC 2700

Qy  2701 ATAAAGTCAGCTGTTAAAATTCAGGTGTGCATGGGTTTCCTTCACGAAGGCCTTTAT 2760
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 ATAAAGTCAGCTGTTAAAATTCAGGTGTGCATGGGTTTCCTTCACGAAGGCCTTTAT 2760

Qy  2761 TTAATGGAATATAGGAGCGAGCTCATTTCCGTAATTCCTAGGCCGTAATTCACGGAAGAGTGAC 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 TTAATGGAATATAGGAGCGAGCTCATTTCCGTAATTCCTAGGCCGTAATTCACGGAAGAGTGAC 2820
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Db 3841 CATTTCAGCGGATGTTTACTATCTGATTCAGAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3901 TAAACAAACACCCAGTTGTAAATGTCTCAGCTTCAGCTTCAAGTTCAGGTTAACTGCCTTA- 3959
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3901 TAAACAAACACCCCATTTGTAAATGTCTCAAGTTCAAGTTCAGGCTTAACTGCCAATCAAAT 3960

Qy 3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTCTCCACATCTGAGGTGAGTCTCGCCAGGG 4019
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTCTCCAC-TCTGAGGTGAGTCTCGCCAGGG 4019

Qy 4020 CAGTTTGGAAATATTTACTTCACAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079

Qy 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTAAAGTTACTTCTGACAGTTTTGGTATA 4139
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTAAAGTTACTTCTGACAGTTTTGGTATA 4139

Qy 4140 TTTATTGGCTATTGCCATTTGCTTTTGTTTTTGTTTTTCTCTTTGGGTTATTAATGTAAAGCA 4199
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4140 TTTATTGGCTATTGCCATTTGCTTTTGTTTTTGTTTTTCTCTTTGGGTTATTAATGTAAAGCA 4199

Qy 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAATTACATTT 4259
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAATTACATTT 4259

Qy 4260 TTGTTTTTACCACCTTCTAACTAAACAGCCCATAAATTTAATTTATTGCGAATAGAGCCATAA 4319
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4260 TTGTTTTTACCACCTTCTAACTAAACAGCCCATAAATTTAATTTATTGCGAATAGAGCCATAA 4319

Qy 4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAATCACAGACAT 4379
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAATCACAGACAT 4379

Qy 4380 TTTATACTATATTACAGTGTTGTGCAGATACGTTGTGTAAGTGAAATATTTATACTCAAAACT 4439
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4380 TTTATACTATATTACAGTGTTGTGCAGATACGTTGTGTAAGTGAAATATTTATACTCAAAACT 4439

Qy 4440 ACTTGAAATTAGACCTCCCGCTGGATCTTGTTTTAACATATTAATAAAACATGTTTAA 4499
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4440 ACTTGAAATTAGACCTCCCGCTGGATCTTGTTTTTTAACATATTAATAAAACATGTTTAA 4499

Qy 4500 AATTTTGATATTTTGATAATCATTCATTATTTGTTCCTTTGTAATCTATATTT 4559
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4500 AATTTTGATATTTTGATAATCATTCATTATTTGTTCCTTTGTAATCTATATTT 4559

Qy 4560 TATATATTTGAAAACATCTTTCTGAGAAGAGAGTTCCCAGATTTCACCATGAGGTTCTTG 4619
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4560 TATATATTTGAAAACATCTTTCTGAGAAGAGAGTTCCCCAGATTTCACCATGAGGTTCTTG 4619

Qy 4620 GCATGCACACACAGAGTAAGAACTGATTGGAGCTAACATTGGCTCTGCCTACGTCTTAAAGGACTTGTT 4679
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4620 GCATGCACACACAGAGTAAGAACTGATTGGAGGGCTAACATTGGCTCGTCCTACGTCTTAAAGGACTTGTT 4679

Qy 4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739

Qy 4740 GAGGGGGGAAATCTGCGCTTCGGGAATGCTCTCCCTGGTAGGGTGCTGT 4799
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db 4740 GAGGGGGGAAATCTGCGCTTCGGGAATGCTCTCCCTGGTAGGGTGCTGT 4799

Qy 4800 CCTTGTGTTCTCGGCTGGCTGTATTTTTCTGTCCCTGTACGTCTTAAAGACTTGTT 4859
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4800 CCTTGTGTTCTCGGCTGGCTGTATTTTTCTGTCCCTGTACGTCTTAAAGACTTGTT 4859

Qy 4860 TGGATCTTCCAGTTCTCCAGCATAGTGCCTGGACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4860 TGGATCTTCCAGTTCTCCAGCATAGTGCCTGGACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919

Qy 4920 GTGAATGGAAATATAAAACTAGAAATATATCCTTGTTGAAATCAGCACCAGTACCCTG 4979
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4920 GTGAATGGAAATATAAAACTAGAAATATATCCTTGTTGAAATCAGCACCAGTACCCTG 4979

Db 2761 TTAATGGGAATATAGGAGCGAGCTCATTTCCTAGGCCGTTAAATTCACGGAAGGAGGTGAC 2820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2821 TGGAGTCTTTCTTCTTTCATGTCTTCTGGGCAACTACTCAGCCTGTGGTGGGACTTGGCTTA 2880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2821 TGGAGTCTTTCTTCTTTCATGTCTTCTGGGCAACTACTCAGCCTGTGGTGGGACTTGGCTTA 2880

Qy 2881 TGCAAGACGGTCGAAAACCTTGGAAATCAGGAGACTCGGTTTCTTCTTCTTGGTTCTGCCATT 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2881 TGCAAGACGGTCGAAAACCTTGGAAATCAGGAGACTCGGTTTCTTCTTCTTGGTTCTGCCATT 2940

Qy 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTCCGGGCCATAGTCTTCTCTCTGCT 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTCCGGGCCATAGTCTTCTCTCTGCT 3000

Qy 3001 ATAAAGAGACCCTTGCAGCTCTCGTGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3001 ATAAAGAGACCCTTGCAGCTCTCGTGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060

Qy 3061 GGATGTTGAGAGGGGAAGGAAGGAGGCAGAGCTGGAGCGCTGAGCCACCAGGGGAGTGGAGGG 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3061 GGATGTTGAGAGGGGAAGGAAGGAGGCAGAGCTGGAGCGCTGAGCCACCAGGGGAGTGGAGGG 3120

Qy 3121 GGACAGGAAGGCAGGCAGAGCTGGGTGCTGCTCCATCAGTCCTACTGACTCACGTCAGACTC 3180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3121 GGACAGGAAGGCAGGCAGAGCTGGGTGCTGCTCCATCAGTCCTACTGACTCACGTCAGACTC 3180

Qy 3181 CAGGACCGAGAGCCAGAGCTCAGGAAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3181 CAGGACCGAGAGCCAGAGCTCAGGAAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240

Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAATAAAGAGATGCAGAGACTAACTGGT 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAGAATGCAGAGACTAACTGGT 3300

Qy 3301 GGTAGCTTTGCCTGGCATTCAAAAACTGGGCCAGAGCCAAGTGGAAAATGCCAGAGATTG 3360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3301 GGTAGCTTTGCCTGGCATTCAAAAACTGGGCCAGAGCCAAGTGGAAAATGCCAGAGATTG 3360

Qy 3361 TTAAACTTTTCACCCTGACCCCCACCCCCACGCACCGGCTGCTGACAGCACGG 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3361 TTAAACTTTTCACCCTGACCCCCACCCCCACGCACCGGCTGCTGACAGCACGG 3420

Qy 3421 AGTGACCTGCACGCCCAGCGCGGGGAGGAGAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3421 AGTGACCTGCACGCCCAGCGCGGGGAGGAGAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480

Qy 3481 ACAGATTCATTCAAGGGCAGTTGGGAATTGACCACAGGGATTATAGTTCCACGTGATCCTGG 3540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTTCCACGTGATCCTGG 3540

Qy 3541 GTTCTCAGGAGGCAGGGGCAATCCCGTTTCTTTCTTTAACAGGAGAAAAATCAGTTCAAGGGAGA 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3541 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTCTTTAACAGGAGAAAAATCAGTTCAAGGGAGA 3600

Qy 3601 CCTGATTTCTAATACTATATTTTTTCCTTTACAAGCTTGAGTAATTCTGAGCAAGTCACAAG 3660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3601 CCTGATTTCTAATACTATATTTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660

Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTCTCTGT 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTCTCTGT 3720

Qy 3721 GTTCTCAGAGGCAGCAGCACAAGGGCAATCCCGTTTCTTTAACAGGAAGAAAACATTCCTAAGAG 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTAACAGGAAGAAAACATTCCTAAGAG 3780

Qy 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840

Qy 3841 CATTTCAGCGGATGTTTACTATCTGATTCAGAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

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Qy    4980  GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGTGAGAT  5039
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4980  GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGTGAGAT  5039

Qy    5040  ATAGGAACTATTATTGGGATGGGTATGGGTCATAAATGGGATGTCTTTTAAAAGAAAACT  5099
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5040  ATAGGAACTATTATTGGGATGGGTATGGGTCATAAATGGGATGTCTTTTAAAAGAAAACT  5099

Qy    5100  CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTGCTGGCAGCGTGAAGGCAACCC  5159
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5100  CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTGCTGGCAGCGTGAAGGCAACCC  5159

Qy    5160  CCCTGTGCACAGCCCCACCCAGGCCTCACGTGCGCCACCTCTGTCTTCCCCATGAGGGGCT  5219
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5160  CCCTGTGCACAGCCCCACCCAGGCCTCACGTGCGCCACCTCTGTCTTCCCCATGAGGGGCT  5219

Qy    5220  GGCTCCCCAGTATATATAAAACCTTCTCTGGAGCTCGGGCATGAGCCAGCCAAGG  5271
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5220  GGCTCCCCAGTATATATAAAACCTTCTCTGGAGCTCGGGCATGAGCCAGCCAAGG  5271
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RESULT 5
US-10-741-339-1
; Sequence 1, Application US/10741339
; Publication No. US2004013279SA1
; GENERAL INFORMATION:
; APPLICANT: Polansky, Jon
; TITLE OF INVENTION: METHODS TO SCREEN AND TREAT INDIVIDUALS WITH GLAUCOMA OR THE PROE
; TITLE OF INVENTION: TO DEVELOP GLAUCOMA
; FILE REFERENCE: 13587.375
; CURRENT APPLICATION NUMBER: US/10/741,339
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 09/985,637
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 1
; LENGTH: 5300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-339-1

Query Match   99.5%; Score 5246.4; DB 7; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5269; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy       1  ATCTTTGTTCAGTTTACCTCAGGGCTATTATGGAAATGAAATGAGATAACCAATGTGAAAG    60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1  ATCTTTGTTCAGTTTACCTCAGGGCTATTATGGAAATGAAATGAGATAACCAATGTGAAAG    60

Qy      61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAGAAATCA   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAGAAATCA   120

Qy     121  GGAAGAAGGAGTATCCACGTTAGCCAAGTTGCCAGGCTGTGTCGTGTTCTTATTTTAGTCA   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121  GGAAGAAGGAGTATCCACGTTAGCCAAGTTGCCAGGCTGTGTCGTGTTCTTATTTTAGTGA   180

Qy     181  CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181  CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC   240

Qy     241  CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCAAGGAAAATGCCAG   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241  CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCAAGGAAAATGCCAG   300

Qy     301  GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTTTAATTTCAGGAAAAAATG   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301  GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTTTAATTTCAGGAAAAAATG   360

Qy     361  ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361  ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG   420

Qy     421  TAATTAAGTATTGTTCCTTGGGAAGAGACCTCCTTCCATGTGAGCTTGATGGGAAAATGGGAA   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421  TAATTAAGTATTGTTCCTTGGGAAGAGACCTCCTTCCATGTGAGCTTGATGGGAAAATGGGAA   480

Qy     481  AAACGTCAAAAGCATGATCAGATCCAAAGTGGATTATTATTTAAAAACCAGAT   540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481  AAACGTCAAAAGCATGATCAGATCCAAAGTGGATTATTATTTAAAAACCAGAT   540

Qy     541  GGCATCACTCCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAGAAGGACATAACAATAAC   600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541  GGCATCACTCCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAGAAGGACATAACAATAAC   600

Qy     601  AGCAAAATCAAAATTCCGACAAATGCAGGAGGAGCAAAAATGGGGACTCGGGGAAAGCTTTCATAAC   660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601  AGCAAAATCAAAATTCCGACAAATGCAGGAGGAGCAAAAATGGGGACTCGGGGAAAGCTTTCATAAC   660

Qy     661  AGTGATTAGGCAGTTGACACTTCGCAACAACCTCCCCGTCTATACCAGGGAACACAAAA   720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661  AGTGATTAGGCAGTTGACACTTCGCAACAACCTCCCCGTCTATACCAGGGAACACAAAA   720

Qy     721  ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATGAAAAAACTGAGAGCAAAACAAAA   780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721  ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATGAAAAAACTGAGAGCAAAACAAAA   780

Qy     781  GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA   840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781  GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA   840

Qy     841  GGGACCCTGAGGCATTTGCCTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC   900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841  GGGACCCTGAGGCATTTGCCTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC   900

Qy     901  TTGAAAGATCATGAATTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG   960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901  TTGAAAGATCATGAATTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG   960

Qy     961  TTTTAGACATGGGTCCCAATTTTATAAATCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961  TTTTAGACATGGGTCCCAATTTTATAAATCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020

Qy    1021  GGATAGGTCAGAAAATCATTAGAAAATCACTGTGTCCCATCCTAACTTTTTCAGAATGATC  1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021  GGATAGGTCAGAAAATCATTAGAAAATCACTGTGTCCCATCCTAACTTTTTCAGAATGATC  1080

Qy    1081  TGTCATAGCCCTCACACAGGCCGATGTGTCTGACCTGACATCTACAACCATCTACAACCCAA  1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081  TGTCATAGCCCTCACACAGGCCGATGTGTCTGACCTGACATCTACAACCATCTACAACCCAA  1140

Qy    1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC  1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC  1200

Qy    1201  TGTGCAGCCCATCCCCGTCTCCCACAGGAAGTCTCCCCACTCAGACTTGCATCACGATGT  1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201  TGTGCAGCCCATCCCCGTCTCCCACAGGAAGTCTCCCCACTCAGACTTGCATCACGATGT  1260

Qy    1261  TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTCTTCACCTACCTAC  1320
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261  TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTCTTCACCTACCTAC  1320

Qy    1321  ACCTGAGCTCACTGCAACCTCTGCCTCTCCCCAGGTTCAAGCAATTCTCTCTGTCTCAGCCTTCC  1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321  ACCTGAGCTCACTGCAACCTCTGCCTCTCCCCAGGTTCAAGCAATTCTCTCTGTCTCAGCCTTCC  1380

Qy    1381  CGGTAGCTGGGACTACAGGCGCACGCCCGGCCTAATTTTTGTATTTTTGTATTGTTAGTAGAGATGG  1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381  CGGTAGCTGGGACTACAGGCGCACGCCCGGCCTAATTTTTGTATTTTTGTATTGTTAGTAGAGATGG  1440

Qy    1441  GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCCACCACCCTC  1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441  GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCCACCACCCTC  1500
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Right-hand (upper) alignment block:

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Qy  2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTCCGTTGCTTCCTGTGAGC 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTCCGTTGCTTCCTGTGAGC 2640

Qy  2641 CTTTTTATCTTTTCTCGCTTGGACGGAGAGAAGTCTATTCATGAAGGATGCAGTTTC 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 CTTTTTATCTTTTCTCGCTTGGACGGAGAGAAGTCTATTCATGAAGGATGCAGTTTC 2700

Qy  2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGCATGGTTTCCTTCACGAAGGCCTTTAT 2760
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGCATGGTTTCCTTCACGAAGGCCTTTAT 2760

Qy  2761 TTAATGGGAATATAGGAAGCGAGCTCATTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 TTAATGGGAATATAGGAAGCGAGCTCATTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820

Qy  2821 TGGAGTCTTTTCTTTCATGTCTTCTGGCAACTACTCAGCCCGTGGTGGACTTGGCTTA 2880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 TTAATGGAGTCTTTTCTTTCATGTCTTCTGGCAACTACTCAGCCCGTGGTGGACTTGGCTTA 2880

Qy  2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTCTTTCTTTCTCGCCATT 2940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 TGCAAGACGTGCGAAAACCTTGGAATCAGGAGACTCGGTTTCTTTCTTTCTCGCCATT 2940

Qy  2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTTCTCCTTCCCGTGTGAACACTTCCCGTGAGTTCTCGTGAGGGG 3000
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTTCTCCTTCCCGTGTGAACACTTCCCGTGAGTTCTCGTGAGGGG 3000

Qy  3001 ATAAAGACCCTGCAGCTCCGTGTTCGTGTTCTGTGAACACTTCCCGTGATTCTCGTGAGGGG 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 ATAAAGACCCTGCAGCTCCGTGTTCGTGTTCTGTGAACACTTCCCGTGATTCTCGTGAGGGG 3060

Qy  3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGGAGCAGGGGAGGTGGAGGG 3120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGGAGCAGGGGAGGTGGAGGG 3120

Qy  3121 GGACAGGAAGGCAGGCAGGCGAAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 GGACAGGAAGGCAGGCAGGCGAAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180

Qy  3181 CAGGACCGGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 CAGGACCGGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240

Qy  3241 TCCCTAAGCATAGACAATGCCATTGCCATTTGCCAATAACCAAAAGAATGCAGAGACTAACTGGT 3300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 TCCCTAAGCATAGACAATGCCATTGCCATTTGCCAATAACCAAAAGAATGCAGAGACTAACTGGT 3300

Qy  3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGCCAGAGATTG 3360
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAATGCCAGAGATTG 3360

Qy  3361 TTAAACTTTTCACCCTGACCAGCACCCCGACGGAGAAGTAGTGTATGAGCAAGAAAG 3420
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 TTAAACTTTTCACCCTGACCAGCACCCCGACTGCTGCAGACACGG 3420

Qy  3421 AGTGACCTGCAGCGCAGGGGAGGAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
         |||||||||||||||||||||||||||||||||||||||||||||
Db  3421 AGTGACCTGCAGCGCAGGGGAGGAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480

Qy  3481 ACAGATTCATTCAAGGCAGCTGGGGGGGTGGGGGAAAAATCAGTTCAACCACGTGATCCTGG 3540
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 ACAGATTCATTCAAGGCAGCTGGGGGGGTGGGGGAAAAATCAGTTCAACCACGTGATCCTGG 3540

Qy  3541 GTTCTAGGAGGCAGGGGTATATTGTGGGGGAGCTTTACAAGCTGAGTAATTCTGAGCAAGGCTCACAAG 3600
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 GTTCTAGGAGGCAGGGGCTATATTGTGGGGGAGCTTTACAAGCTGAGTAATTCTGAGCAAGGCTCACAAG 3600

Qy  3601 CCTGATTTCTAATACTATATTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGGCTCACAAG 3660
         |||||||||||||||||||||||||||||||||||||||||||||
Db  3601 CCTGATTTCTAATACTATATTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGGCTCACAAG 3660

Qy  3661 GTAGTAACTGAGCGTGTAAGAATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCGT 3720
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Left-hand (lower) alignment block:

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Qy  1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACGCGCCCGCCAAGGGTCAGTGT 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACGCGCCCGCCAAGGGTCAGTGT 1560

Qy  1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGAGGGAAACAGACAAAAGCTGTGA 1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGAGGGAAACAGACAAAAGCTGTGA 1620

Qy  1621 TAATTTCAGGGATTCTTGGGATGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 TAATTTCAGGGATTCTTGGGATGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680

Qy  1681 CACTGTCCTCATCACTTTCTTCTTCCCTCATCCTCAGGCTAAGTTACCATTTTATT 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 CACTGGTCCTCATCACTTTCTTCTTCCCTCATCCTCAGGCTAAGTTACCATTTTTATT 1740

Qy  1741 CACCATGCTTTTGTGTGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 CACCATGCTTTTGTGTGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy  1801 TTCCATTTGGGGCCATCGTGTGTGTGTGTATAGGGGAGGGGCATACCCCAGGACTCCT 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 TTCCATTTGGGGCCATCGTGTGTGTGTGTATAGGGGAGGGGCATACCCCAGGACTCCT 1860

Qy  1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGTGGGGAGCCCTGGAGCACCCGGGGTCC 1920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 TGAGCCGTGCGACCGTGGGCAAGCCCTGGAGCACCCGGGGTCC 1920

Qy  1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTGTTATCACTCTCTAGG 1980
         |||||||||||||||||||||||||||||||||||||||||||||
Db  1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTGTTATCACTCTCTAGG 1980

Qy  1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATTCATTCCAGGCATTCATTGACAATT 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATTCATTCCAGGCATTCATTGACAATT 2040

Qy  2041 TATTGAGTACTTATATCTGCCAGACACCCAGAGACAAAATGTGAGCAAAGCAGTCACTGC 2100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 TATTGAGTACTTATATCTGCCAGACACCCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy  2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATAATAGCCA 2160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATAATAGCCA 2160

Qy  2161 GCCAACTTAAACCCAGTCGTCCGTGAATCGTCCGTGTCATCGATCTTGAGAATTGTGTCGGC 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCCAACTTAAACCCAGTCGTCCGTGAATCGTCCGTGTCATCGATCTTGAGAATTGTGTCGGC 2220

Qy  2221 AGCATCCCTAACAAGGCCACTTCCCTAGCGCCCCCCTCCGTGCCCGGAGG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 AGCATCCCTAACAAGGCCACCTCCCTAGCGCCCCCCTCCGTGCCCGGAGG 2280

Qy  2281 CCCCAAGCCCGGAGTCTTCCAAGCCTCCTCCTCCATCAGCTCACCAGCGCTGCAGCTGGCCT 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 CCCCCAAGCCCGGAGTCTTCCAAGCCTCCTCCTCCATCAGCTCACCAGCGCTGCAGCTGGCCT 2340

Qy  2341 GCCTCGCTTCCCGTGAATCGTCCGTGAATCGTCGGAGACTCCTTGGCTTCCAGGCT 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 GCCTCGCTTCCCGTGAATCGTCCGTGAATCGTCGGAGACTCCTTGGCTTCCAGGCT 2400

Qy  2401 CCAGAAAGGAAATGGAGAGGGGGCCTCACGTCGGGGAAACTCGGAGAGATCTGGAGGGGACAGTGTTTC 2460
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 CCAGAAAGGAAATGGAGAGGGGGCCTCCACGTCGGGGAAACTCGGAGAGATCTGGAGGGGACAGTGTTTC 2460

Qy  2461 CTTCAGAGGGAAAGGGCTGGGGCTGAGCGGGGCTGAGCGCTGAAAGGCAGGGGGTGAAAAGGGCAAGGCTGAA 2520
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CTTCAGAGAGGGAAAGGGCTGGGGCTGAGCGGGGCTGAGCGCTGAAAGGCAGGGGGTGAAAAGGGCAAGGCTGAA 2520

Qy  2521 TGGGGACGGCTGGGGCTGAGCGGGGCTGAGCGCTGAAAGGCAGGAAGGCAGGAAGGGCAAGGCTGAA 2580
         |||||||||||||||||||||||||||||||||||||||||||||
Db  2521 TGGGGACGGCTGGGGCTGAGCGGGGCTGAGCGCTGAAAGGCAGGAAGGCAGGAAGGGCAAGGCTGAA 2580
```

Db   4740 GAGGGGGGAAATCTGCCGCGTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4800 CCTTGTGTTCGCGGCTGGCTGTCGTGTATTTTCTGTCGTCCTGCTCACGTCTTAAAGGACTTGTT 4859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4800 CCTTGTGTTCGCGGCTGGCTGTCGTGTATTTTCTGTCGTCCTGCTCACGTCTTAAAGGACTTGTT 4859

Db   4860 TGGATCTCCAGTTCCTAGACTATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTGCAGA 4919
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4860 TGGATCTCCAGTTCCTAGACTATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTGCAGA 4919

Qy   4920 GTGAATGGAAATATAAACTAGAAATATATCCTGTGAAATCAGCACACCAGTAGTCCTG 4979
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTGAAATCAGCACACCAGTAGTCCTG 4979

Qy   4980 GTGTAAGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGGATGTTCTTTTAAAAGAAACT 5039
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4980 GTGTAAGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGGATGTTCTTTTAAAAGAAACT 5039

Qy   5040 ATAGGAACTATTATTGGGTATGGGTCATAAATTGGGATGTTCTTTTAAAAGAAACT 5099
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5040 ATAGGAACTATTATTGGGTATGGGTCATAAATTGGGATGTTCTTTTAAAAGAAACT 5099

Qy   5100 CCAAACAGACTTCTGGAAGTTATTTTCTAGAAATCTTGCTGGCAGGTGAAGGCAACCC 5159
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5100 CCAAACAGACTTCTGGAAGTTATTTTCTAGAAATCTTGCTGGCAGGTGAAGGCAACCC 5159

Qy   5160 CCCTGTGCACAGCCCCACCCCACCTCGCTCTTCCCCATGAGCCAGCAAGG 5219
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5160 CCCTGTGCACAGCCCCACCCCACCTCGCTCTTCCCCATGAGCCAGCAAGG 5219

Qy   5220 GGCTCCCAGTATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271

RESULT 6
US-10-087-192-1228
; Sequence 1228, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 52945200122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1228
; LENGTH: 37252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-1228

Query Match   99.3%; Score 5232.4; DB 5; Length 37252;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5267; Conservative 0; Mismatches 1; Indels 4; Gaps 3;

Qy   1 ATCTTTGTTCAGTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4731 ATCTTTGTTCAGTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 4790

Qy   61 TCCTATAAACTGTATAGCCTCCATTCGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4791 TCCTATAAACTGTATAGCCTCCATTCGATGTATGTCTTTGGCAGGATGATAAAGAATCA 4850

Qy   121 GGAAGAGGAGTATCCACGTTAGCCAAGTGGTCGTCTGCTCTTATTTTAGTTGA 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   3661 ....
             ||||||||||
Qy   3661 GTAGTAACTGAGGCGTGTAAGACTACTTAGTTGTTCTCCTTATTAGGAACTCTTTCTCTGT 3720

Db   3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTCTTCTTTAAACAGGAAGAAAACATTCCTAAGAG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTCTTCTTTAAACAGGAAGAAAACATTCCTAAGAG 3780

Db   3781 TAAAGCCAAACAGATTCAAGCCTAGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3781 TAAAGCCAAACAGATTCAAGCCTAGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840

Qy   3841 CATTTCAGCGGATGTGTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 CATTTCAGCGGATGTTTACTATCTGATTCAGAAAATGAGAACTAGTACCCTTTGGTCAGCTG 3900

Qy   3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 TAAACAAACACCCCATTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 3960

Qy   3960 AAGAATAGAATCTTTAGAGACAAACTGTGTTCTCCACATCTGGAGGTGAGTCGTCTGCCAGGG 4019
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 AAGAATAGAATCTTTAGAGACAAACTGTGTTCTCCAC-TCTGGAGGTGAGTCGTCTGCCAGGG 4019

Qy   4020 CAGTTTGGAAATATTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4020 CAGTTTGGAAATATTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079

Db   4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTAAAGTTACTTCTGACAGTTTTGTATA 4139
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTAAAGTTACTTCTGACAGTTTTGTATA 4139

Qy   4140 TTTATTGGCTATTGCCATTTGCTTTTGTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4140 TTTATTGGCTATTGCCATTTGCTTTTGTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199

Qy   4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGAATTGAATGAGGAAAAAATTACATTT 4259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGAATTGAATGAGGAAAAAATTACATTT 4259

Qy   4260 TTGTTTTTACCACCTTCTAACACTTTCTAACATTTATTAACATTTATTCCATTGCGAATAGAGCCATAA 4319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4260 TTGTTTTTACCACCTTCTAACACTTTCTAACATTTAA-CATTTATTCCATTGCGAATAGAGCCATAA 4319

Qy   4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTGTCATTAGTTGTCATTACCAATGAAATCACAGACAT 4379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4320 ACTCAAAGTGTGAATAACAGTACCTGTGATTTGTCATTAGTTGTCATTACCAATGAAATCACAGACAT 4379

Qy   4380 TTTATACTATATTACAGTTGTGCAGATACGTTGAAGTGAAATATTTATACTCAAAACT 4439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4380 TTTATACTATATTACAGTTGTGCAGATACGTTGAAGTGAAATATTTATACTCAAAACT 4439

Qy   4440 ACTTTGAAATTTAGACCTCCCTGCTGGATCTTGTTTTTTAACATATTAATAAACATGTTTAA 4499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4440 ACTTTGAAATTTAGACCTCCCTGCTGGATCTTGTTTTTTAACATATTAATAAACATGTTTAA 4499

Qy   4500 AATTTTGAAATTTGATAATCATCTTTGTTCCTTTGTAATCTATATTT 4559
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db   4500 AATTTTGAAATTTGATAATCATCTTTGTTCCTTTGTAATCTATATTT 4559

Qy   4560 TATATATTTGAAAAACATCTTTCTGAGAGAGTTCCCCAGATTTCACCAATTGGTTCTTG 4619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4560 TATATATTTGAAAAACATCTTTCTGAGAGAGTTCCCCAGATTTCACCAATTGGTTCTTG 4619

Qy   4620 GCATGCACACACAGAGTAAGCAACATTGACATTGGTGCCTGAG 4679
             |||||||||||||||||||||||||||||||||||||||||||
Db   4620 GCATGCACACACAGAGTAAGCAACATTGACATTGGTGCCTGAG 4679

Qy   4680 ATGCCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGGT 4739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4680 ATGCCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGGT 4739

Qy   4740 GAGGGGGGAAATCTGCCGCGTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db  4851 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTCTCTTATTTTAGTGA 4910
                                                                              Qy  1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
                                                                                        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  5991 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 6050

Qy   181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4911 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 4970
                                                                              Qy  1321 ACCTGAGCTCACTGCAACCTCGCCTCCCCAGGTTCAAGCAATTCCTCGTGTCTCAGCCTCC 1380
                                                                                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  6051 ACCTGAGCTCACTGCAACCTCTGCCTCCCCAGGTTCAAGCAATTCCTCGTGTCTCAGCCTCC 6110

Qy   241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCGAG 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4971 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 5030
                                                                              Qy  1381 CGGGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTGTATTGTTAGTAGGAGATGGG 1440
                                                                                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  6111 CGGGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTGTATTGTTAGTAGGAGATGGG 6170

Qy   301 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTGTTTTAATTTCAGGAAAAAATG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5031 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTAATTTCAGGAAAAAATG 5090
                                                                              Qy  1441 GTTTCACCATATTAGCCCGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
                                                                                        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  6171 GTTTCACCATATTAGCCCGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 6230

Qy   361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAGATGTTTCCAAATTGG 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5091 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAGATGTTTCCAAATTGG 5150
                                                                              Qy  1501 AGCCTCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
                                                                                        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  6231 AGCCTCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 6290

Qy   421 TAATTAAGTATTTGTTCCTTGTGGAAGAGACTTGGGAAAATGGGAA 480
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  5151 TAATTAAGTATTTGTTCCTTGTGGAAGAGACTTGGGAAAATGGGAA 5210
                                                                              Qy  1561 TTAATAAGGAATAACTTGAAATGGTTTACTAAACAACAGGAAACAGACAAAAGCTGTGA 1620
                                                                                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  6291 TTAATAAGGAATAACTTGAAATGGTTTACTAAACAACAGGAAACAGACAAAAGCTGTGA 6350

Qy   481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTTATTATATTTTAAAAACCAGAT 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5211 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTTATTATATTTTAAAAACCAGAT 5270
                                                                              Qy  1621 TAATTTCAGGGATTCTTCGGAATGGGGATGGGATGGGATGCTGCCCAGTGTCCCCAGAC 1680
                                                                                        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  6351 TAATTTCAGGGATTCTTCGGAATGGGGATGGGATGGGATGCTGCCCAGTGTCCCCAGAC 6410

Qy   541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGTTAGCAAAGGACATAACAATAAC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5271 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGTTAGCAAAGGACATAACAATAAC 5330
                                                                              Qy  1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTCAGGCTAAGTTACCATTTTATT 1740
                                                                                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  6411 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTCAGGCTAAGTTACCATTTTATT 6470

Qy   601 AGCAAAATCAAAATTCCGCAAAATGCAGGAGGAAAATGGGACTTGGGAAAGCTTTCATAAC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5331 AGCAAAATCAAAATTCCGCAAAATGCAGGAGGAAAATGGGACTTGGGAAAGCTTTCATAAC 5390
                                                                              Qy  1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
                                                                                        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  6471 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 6530

Qy   661 AGTGATTAGGCAGTGCAACCATGTTGCGCAACACCTCCCCGTCTATACACAGGGAACACAAAA 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5391 AGTGATTAGGCAGTGCAACCATGTTGCGCAACACCTCCCCGTCTATACACCAGGGAACACAAAA 5450
                                                                              Qy  1801 TTCCATTTGGGGCCATCGTGTGTGTATAGGGAGGAGGGCATACCCCAGAGACTCCT 1860
                                                                                        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  6531 TTCCATTTGGGGCCATCGTGTGTGTATAGGGAGGAGGGGCATACCCCAGAGACTCCT 6590

Qy   721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAATCAGAGCACAACAAAA 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5451 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCACAACAAAA 5510
                                                                              Qy  1861 TGAAGCCCCGGCAGAGGTTTCCTCTCCTCCGAGCTCGGGGAGCCCTGCAGCACCCGGGGTCC 1920
                                                                                        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  6591 TGAAGCCCCGGCAGAGGTTTCCTCTCCTCCGAGCTCGGGGAGCCCTGCAGCACCCGGGGTCC 6650

Qy   781 GACATGGTTAAAAGGCAACCAGAGACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5511 GACATGGTTAAAAGGCAACCAGAGACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 5570
                                                                              Qy  1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTTCTAGG 1980
                                                                                        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  6651 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTTCTAGG 6710

Qy   841 GGGACCCTGAGGCATTTGCCTTTAGGAGGCCAGTTTTCTTAGGAATCTTAAGAAACTC 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5571 GGGACCCTGAGGCATTTGCCTTTAGGAGGCCAGTTTTCTTAGGAATCTTAAGAAACTC 5630
                                                                              Qy  1981 GACCTGTTGCTTTCTATTTCTCGTGACTCGTCATTCATCAGGCATTCATTGACAATT 2040
                                                                                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  6711 GACCTGTTGCTTTCTATTTCTCGTGACTCGTCATTCATCAGGCATTCATTGACAATT 6770

Qy   901 TTGAAAGATCATGAATTTAACCATTTTAAGTATAAAACAAATATGGCATGCATAATCAG 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5631 TTGAAAGATCATGAATTTAACCATTTTAAGTATAAAACAAATATGGCATGCATAATCAG 5690
                                                                              Qy  2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
                                                                                        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  6771 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 6830

Qy   961 TTTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5691 TTTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 5750
                                                                              Qy  2101 CCTACCTTCGTGAGGTGACAGTTCTCATGAAGACGTGCGAAGAGAAAATTAATAGCCA 2160
                                                                                        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  6831 CCTACCTTCGTGAGGTGACAGTTCTCATGAAGACGTGCGAAGAGAAAATTAATAGCCA 6890

Qy  1021 GGATAGGTCAGAAATCATTAGGAAATCACTGTGTCCCATCCTAACTTTTCAGGAATGATC 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5751 GGATAGGTCAGAAATCATTAGGAAATCACTGTGTCCCATCCTAACTTTTCAGGAATGATC 5810
                                                                              Qy  2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGGC 2220
                                                                                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  6891 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 6950

Qy  1081 TGTCATAGCCCTCACACAGCCCGATGTGTCTGACCTACAACCATCTACAACCCAA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5811 TGTCATAGCCCTCACACAGCCCGATGTGTCTGACCTACAACCATCTACAACCCAA 5870
                                                                              Qy  2221 AGCATCCCTTAACAAGGCCACCTCCTAGCGCCCTCGCTCCTCCATCGTTGCCGAGG 2280
                                                                                        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  6951 AGCATCCCTTAACAAGGCCACCTCCTAGCGCCCTCGCTCCTCCATCGTTGCCGAGG 7010

Qy  1141 GTGTTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCATTACAAATGCCACCTCCCC 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5871 GTGTTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCATTACAAATGCCACCTCCCC 5930
                                                                              Qy  2281 CCCCAAGCCCGAGTCTTCCAAGCCTCCTCCATCAGTCACAGCTCACCAGCGCTGGCCT 2340
                                                                                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                              Db  7011 CCCCAAGCCCGAGTCTTCCAAGCCTCCTCCATCAGTCACAGCTCACCAGCGCTGGCCT 7070

Qy  1201 TGTGCAGCCCATCCCGCTCCACAGGAGAGTCTTCCCCACTCTAGACTTCTGCATCACGATGT 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5931 TGTGCAGCCCATCCCGCTCCACAGGAGAGTCTTCCCCACTCTAGACTTCTGCATCACGATGT 5990
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Qy 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTCATCTGAGCTGAGACTCCTTGGCTCCAGGCT 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7071 GCCTCGCTTCCCGTGAATCGTCCTGGTCATCTGAGCTGAGACTCCTTGGCTCCAGGCT 7130

Qy 2401 CCAGAAAGGAAATGAGAGGGAAACTAGTCTAACGGAGAATCTAACGGAGAATCTGAGGGA 2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7131 CCAGAAAGGAAATGAGAGGGAAACTAGTCTAACGGAGAATCTAACGGAGAATCTGAGGGA 7190

Qy 2461 CTCAGAGGAGGAAAGGGGCCTCCACGTCCAGAGAATTCCAGGAGGTGGGACTGCAGGGAG 2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7191 CTCAGAGGAGGAAAGGGGCCTCCACGTCCAGAGAATTCCAGGAGGTGGGACTGCAGGGAG 7250

Qy 2521 TGGGGACGCTGGGCGCTGAGCGGCTGAGCCTGAAAAGGCAGGAAGTGAAAAGGCAAGGCTGAA 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7251 TGGGGACGCTGGGCGCTGAGCGGCTGAGCCTGAAAAGGCAGGAAGTGAAAAGGCAAGGCTGAA 7310

Qy 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGCGGCTGGGAGTTTCCGTTGCCTTCCTGTGAGC 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7311 GCTGCCCAGATGTTCAGTGTTGTTCACGCGGCTGGGAGTTTCCGTTGCCTTCCTGTGAGC 7370

Qy 2641 CTTTTATCTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7371 CTTTTATCTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 7430

Qy 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTCCTTCACGAAGGCCTTTAT 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7431 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTCCTTCACGAAGGCCTTTAT 7490

Qy 2761 TTAATGGAATATAGGAAGCGAGCTCATTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7491 TTAATGGGAATATAGGAAGCGAGCTCATTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 7550

Qy 2821 TGGAGTCTTTTCATGTCTTCTGGCAACTACTCAGCCCGTGTGTGACTTGGCTTA 2880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7551 TGGAGTCTTTTCATGTCTTCTGGCAACTACTCAGCCCGTGTGTGACTTGGCTTA 7610

Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTCTTTCTGGTTCTGTTCTGGTTCTGCCATT 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7611 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTCTTTCTGGTTCTGTTCTGGTTCTGCCATT 7670

Qy 2941 GGTTGGCTGCGTGCGACCCGTGGGCAAGTGTCTCCCTTCCCTGGGCCATAGTCTCTCGCT 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7671 GGTTGGCTGCGTGCGACCCGTGGGCAAGTGTCTCCCTTCCCTGGGCCATAGTCTCTCGCT 7730

Qy 3001 ATAAAGACCCCTGCAGCTCTCAGTCTTCGTGTTCTGTGAACACTTCCCGTGATTCTGTGTGAGGGG 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7731 ATAAAGACCCCTGCAGCTCTCAGTCTTCGTGTTCTGTGAACACTTCCCGTGATTCTGTGTGAGGGG 7790

Qy 3061 GGATGTTGAGAGGGGGAAGGAGGAGCAGAGCTGGAGCAGCTGGACCACCAGTCCTCCATCAGTGAGCCACAGGAGGTGGAGGG 3120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7791 GGATGTTGAGAGGGGGAAGGAGGAGCAGAGCTGGAGCAGCTGGACCACCAGTCCTCCATCAGTGAGCCACAGGAGGTGGAGGG 7850

Qy 3121 GGACAGGAAGGCAGGCAGGCAGCAGGAAGCTGGGGTGCTCCAATAACCAACCCAGATGAACCCAACAGCCACATTTCCT 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7851 GGACAGGAAGGCAGGCAGGCAGCAGGAAGCTGGGGTGCTCCAATAACCAACCCAGATGAACCCAACAGCCACATTTCCT 7910

Qy 3181 CAGGAGGCATAGAACAATGCTGGCATTTGCCAATTGCCAATAACTGGGCCAGAAAGAATGCAGAGACTAACTGGT 3240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7911 CAGGAGGCATAGAACAATGCTGGCATTTGCCAATTGCCAATAACTGGGCCAGAAAGAATGCAGAGACTAACTGGT 7970

Qy 3241 TCCCTAAGCATGAACAATGGGCATTGCCAATAACCGGCCAGAAAGACTCCACTAACAGCACAGACT 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7971 TCCCTAAGCATGAACAATGGGCATTGCCAATAACCGGCCAGAAAGACTCCACTAACAGCACAGACT 8030

Qy 3301 GGTAGCTTTTGCCTGCCATTCAAAAACTGGGCCAGAGCTGGCAAGTGGAAAATGCCAGAGATTG 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8031 GGTAGCTTTTGCCTGCCATTCAAAAACTGGGCCAGAGCTGGCAAGTGGAAAATGCCAGAGATTG 8090

Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCGAGTCGACTGACAGCACGG 3420
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db 8091 TTAAACTTTTCACCCTGACCAGCACCCCACGCGAGTCGACTGACAGCACGG 8150

Qy 3421 AGTGACCTGCAGCGCGCAGGGGAGGAGAAAGAGAGGGATAGTGTATGAGCAAGAAAAG 3480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8151 AGTGACCTGCAGCGCGCAGGGGAGGAGAAAGAGAGGGATAGTGTATGAGCAAGAAAAG 8210

Qy 3481 ACAGATTCATTCAAGGCAGTGGAATTGACCACCAGGGATTATAGTGCACGTGATCCTGG 3540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8211 ACAGATTCATTCAAGGCAGTGGAATTGACCACCAGGGATTATAGTGCACGTGATCCTGG 8270

Qy 3541 GTTCTAGGAGGCAGGGCTATATGTGGGGGGAAAAAATCAGTTCAAGGGGAGTCGGGAGA 3600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8271 GTTCTAGGAGGCAGGGCTATATGTGGGGGGAAAAAATCAGTTCAAGGGGAGTCGGGAGA 8330

Qy 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8331 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 8390

Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAGAACTCTTTTCTCTGT 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8391 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAGAACTCTTTTCTCTGT 8450

Qy 3721 GGAGGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAGAGAG 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8451 GGAGGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 8510

Qy 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTAGCTATATGATTGGTTTTTTGAAAAAT 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8511 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTAGCTATATGATTGGTTTTTTGAAAAAT 8570

Qy 3841 CATTTCAGCGACGATGTTTACTATGTCTGATTCAGAAAATGAGACTAGTACCCTTGGTCAGCTG 3900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8571 CATTTCAGCGACGATGTTTACTATGTCTGATTCAGAAAATGAGACTAGTACCCTTGGTCAGCTG 8630

Qy 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8631 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 8690

Qy 3960 AAGAATAGAATCTTTAGAGCAAAACTGTGTTTCTCCACATCGGAGGTGAGTCTGCCAGGG 4019
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8691 AAGAATAGAATCTTTAGAGCAAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 8749

Qy 4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTGTTGGTATTAACAACATAAAG 4079
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8750 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTGTTGGTATTAACAACATAAAG 8809

Qy 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTAAAGTTACTTCTGACAGTTTGGTATA 4139
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8810 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTAAAGTTACTTCTGACAGTTTGGTATA 8869

Qy 4140 TTTATTGGCTATTGCCATTTGCCATTTGTCTTTTTGTTTTTGTTTTTCTCTTTGGGTTATTAATGTAAAGCA 4199
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8870 TTTATTGGCTATTGCCATTTGCCATTTGTCTTTTTGTTTTTGTTTTTCTCTTTGGGTTATTAATGTAAAGCA 8929

Qy 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTGAATGAGAGAAAATTACATTT 4259
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8930 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTGAATGAGAGAAAAATTACATTT 8989

Qy 4260 TTGTTTTTACCACCTTCTAACTAAATTAACAGTACCTTGTCATTTATTCCATTGCGAATAGAGCCATAA 4319
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8990 TTGTTTTTACCACCTTCTAACTAAATTAACAGTACCTTGTCATTTATTCCATTGCGAATAGAGCCATAA 9049

Qy 4320 ACTCAAAGTGTAATAACAGTGTAATTTTAACATATTTAATAAAACATGTTTAA 4379
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9050 ACTCAAAGTGTAATAACAGTGTAATTTTAACATATTTAATAAAACACAGACAT 9109

Qy 4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTGAAGTAAGTAAACATGTTTAA 4439
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9110 TTTATACTATATTACAGTTGTTGCAGATACGTTGTGAAGTAAGTAAACATGTTTAA 9169

Qy 4440 ACTTTGAAATTAGAACCTTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9170 ACTTTGAAATTAGAACCTTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 9229

Qy 4500 AATTTTGATAATTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTTAATCTATATTT 4559
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
; LENGTH: 5304
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-633-2

Query Match        99.1%;    Score 5224.4;    DB 5;    Length 5304;
Best Local Similarity   99.8%;    Pred. No. 0;
Matches 5264;  Conservative  0;  Mismatches  0;  Indels  6;  Gaps  3;

Qy      1 ATCTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy     61 TCCTATAAACTGTATAGCCTCCATTGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCTATAAACTGTATAGCCTCCATTGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy    121 GGAAGAAGGAGTATCCAGTTAGCCAAGTGTCCAAGTGCTGTGTCTTGCTCTTTATTTTAGTGA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGAAGAAGGAGTATCCAGTTAGCCAAGTGTCCAAGTGCTGTGTCTTGCTCTTTATTTTAGTGA 180

Qy    181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAAACATCACATCAATATGGTAAATC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCAATATGGTAAATC 240

Qy    241 CATCAAACAGGAGCTAAGAAACACAGGAATGAGATGGGCACTGCCCAAGAAAAAATGCCAG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CATCAAACAGGAGCTAAGAAACACAGGAATGAGATGGGCACTGCCCAAGAAAAAATGCCAG 300

Qy    301 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTAATTTCAGGAAAAAATG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTAATTTCAGGAAAAAATG 360

Qy    361 ATAGGAGACCAAAATCAATGAATAAGGAAAAACAGCTCAGAAAAAGAGATGTTCCAAATTGG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATAGGAGACCAAAATCAATGAATAAGGAAAAACAGCTCAGAAAAAGAGATGTTCCAAATTGG 420

Qy    421 TAATTAAGTATTGTTCCTTGGGAAGAGCACCTCCATGTGAGCTGATGGGAAAATGGGAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TAATTAAGTATTGTTCCTTGGGAAGAGCACCTCCATGTGAGCTGATGGGAAAATGGGAA 480

Qy    481 AAACGTCAAAAGCATGATCATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAACGTCAAAAGCATGATCATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy    541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGTTCATGTTAGCAAAGGACATAACAATAAC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGTTCATGTTAGCAAAGGACATAACAATAAC 600

Qy    601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy    661 AGTGATTAGGCAGTTGCCATGTTGACCATGTTCGCAACACCTCCCGTCTATACCAGGGAACACCAAAA 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGTGATTAGGCAGTTGCCATGTTGACCATGTTCGCAACACCTCCCGTCTATACCAGGGAACACCAAAA 720

Qy    721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy    781 GACATGGTAAAAGCAACAGCAACATTGTGAGCCTTCAAAGCAGCCTTCAAAAGCAGTGCCCCTCAGCA 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GACATGGTAAAAGCAACAGCAACATTGTGAGCCTTCAAAGCAGCCTTCAAAAGCAGTGCCCCTCAGCA 840

Qy    841 GGGACCCTGAGGCATTGCCTTTAGGAAGGCCAGTTTCTTAAGGAATCTTAAGAAACTC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGGACCCTGAGGCATTGCCTTTAGGAAGGCCAGTTTCTTAAGGAATCTTAAGAAACTC 900

Qy    901 TTGAAAGATCATGAATTTAACCATTTTAAGTATAAAAACAAAATATGCCGATGCATAATCAG 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TTGAAAGATCATGAATTTAACCATTTTAAGTATAAAAACAAAATATGCCGATGCATAATCAG 960
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Db   9230 AATTTTGATATTTTGATAATCATATTTCATTATCATTGTTCCTTTGTAATCTATATTT 9289
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4560 TATATATTTGAAAACATCTTCTGAGAGAGTTCCCCAGATTCACCAATGAGGTTCTTG 4619
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9290 TATATATTTGAAAACATCTTCTGAGAGAGTTCCCCAGATTCACCAATGAGGTTCTTG 9349

Qy   4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9350 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 9409

Qy   4680 ATGCAAGACTGAAATTAGAAAGTTCTCCAAAGATACACAGTTGTTTAAAGCTAGGGGT 4739
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9410 ATGCAAGACTGAAATTAGAAAGTTCTCCAAAGATACACAGTTGTTTAAAGCTAGGGGT 9469

Qy   4740 GAGGGGGGAAATCTGCCGCCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9470 GAGGGGGGAAATCTGCCGCCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 9529

Qy   4800 CCTTGTGTTCTCGGCTGGCTGTGTTATTTTCTCGTGTCCTGCTACGTCTTAAAGGACTTGTT 4859
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9530 CCTTGTGTTCTCGGCTGGCTGTGTTATTTTCTCGTGTCCTGCTACGTCTTAAAGGACTTGTT 9589

Qy   4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9590 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 9649

Qy   4920 GTGAATGGAAAATAAAACTAGAAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9650 GTGAATGGAAAATAAAACTAGAAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 9709

Qy   4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTATGGTGCATAAATTGGGAGTGTCATAAAAGAAACT 5039
            |||||||||||||||||||||         |||||||||||||||||||||||||||||
Db   9710 GTGTAAGTGTGTGTAC--GTGTGTGTGTGTGTGTGATGGTGCATAAATTGGGAGTGTCATAAAAGAAACT 9767

Qy   5040 ATAGGAACTATTATTGGGGTATGGTGCATAAATTGGGAGTGTTCTTTTAAAAAGAAACT 5099
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9768 ATAGGAACTATTATTGGGGTATGGTGCATAAATTGGGAGTGTTCTTTTAAAAAGAAACT 9827

Qy   5100 CCAAACAGACTTCTGGAAGGTTATTTCTAAGAAATCTTGCTCGGCCAGCGTGAAGGCAACCC 5159
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9828 CCAAACAGACTTCTGGAAGGTTATTTCTAAGAAATCTTGCTCGGCCAGCGTGAAGGCAACCC 9887

Qy   5160 CCCTGTGCACAGCCCCACCCCAGCCTCAGTGGCCACCTCGTCTTCCCCATGAAGGGCT 5219
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9888 CCCTGTGCACAGCCCCACCCCAGCCTCAGTGGCCACCTCGTCTTCCCCATGAAGGGCT 9947

Qy   5220 GGCTCCCCAGTATATATAAACCTTCTCTGGAGCTCGGGGATGAGCGCAGCAAGG 5271
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   9948 GGCTCCCCAGTATATATAAACCTTCTCTGGAGCTCGGGGATGAGCGCAGCAAGG 9999
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RESULT 7
US-10-244-633-2
; Sequence 2, Application US/10244633
; Publication No. US20030068640A1
; GENERAL INFORMATION:
;   APPLICANT: Nguyen, Thai D.
;   APPLICANT: Polansky, Jon R.
;   APPLICANT: Chen, Pu
;   APPLICANT: Chen, Hua
;   TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
;   TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
;   TITLE OF INVENTION: Disorders
;   FILE REFERENCE: 07425.0057.US01
;   CURRENT APPLICATION NUMBER: US/10/244,633
;   CURRENT FILING DATE: 2002-09-17
;   PRIOR APPLICATION NUMBER: US/09/306,828
;   PRIOR FILING DATE: 1999-05-07
;   PRIOR APPLICATION NUMBER: US 09/227,881
;   PRIOR FILING DATE: 1999-01-11
;   NUMBER OF SEQ ID NOS: 38
;   SOFTWARE: Microsoft Word 97
; SEQ ID NO 2

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Qy    961  TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020

Qy   1021  GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTCAGATGATGATC  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTCAGATGATGATC  1080

Qy   1081  TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA  1140

Qy   1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGTCCCATTACAAATGCCACCTCCCC  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGTCCCATTACAAATGCCACCTCCCC  1200

Qy   1201  TGTGCAGCCCATCCGCTCCACAGGAGTCTCCCCACTCTTCGATCTTTCGATCACGATGT  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  TGTGCAGCCCATCCGCTCCACAGGAGTCTCCCCACTCTTCGATCTTTCGATCACGATGT  1260

Qy   1261  TACAGCCAGAAGTCCGTGAGGGTGAGGGTCTTACACCTACCTGTATGCTCTAC  1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  TACAGCCAGAAGTCCGTGAGGGTGAGGGTCTTACACCTACCTGTATGCTCTAC  1320

Qy   1321  ACCTGAGCTCACTGCAACCTCTGCCTCCAGGTTCAAGCAATTCTCTGTCTCAGCCTCC  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  ACCTGAGCTCACTGCAACCTCTGCCTCCAGGTTCAAGCAATTCTCTGTCTCAGCCTCC  1380

Qy   1381  CGGCTAGTCGGGGACTACAGGCGCACCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG  1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CGGCTAGTCGGGGACTACAGGCGCACCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG  1440

Qy   1441  GTTTCACCATATTAGCCCGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC  1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  GTTTCACCATATTAGCCCGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC  1500

Qy   1501  AGCCTCCTCCAAAGTGCTGGGATTACAGGCATGAGTCACCGCCGCCCGGCCCAAGGGTCAGTGT  1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  AGCCTCCTCCAAAGTGCTGGGATTACAGGCATGAGTCACCGCCGCCCGGCCCAAGGGTCAGTGT  1560

Qy   1561  TTAATAAGGAATAACTTGAATGGTTACTAAACCAACAGAGAAAACAGACAAAAGCTGTGA  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  TTAATAAGGAATAACTTGAATGGTTACTAAACCAACAGAGAAAACAGACAAAAGCTGTGA  1620

Qy   1621  TAATTTCAGGGATTCTTGGGAATGGTGGGAATGGCCATGAGCTGCCTAGTCCCAGAC  1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  TAATTTCAGGGATTCTTGGGAATGGTGGGAATGGCCATGAGCTGCCTAGTCCCAGAC  1680

Qy   1681  CACTGGTCCTCATCACTTTCTTCCCTCATTTCAGGCTAAGTTACCATTTTATT  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  CACTGGTCCTCATCACTTTCTTCCCTCATTTCAGGCTAAGTTACCATTTTATT  1740

Qy   1741  CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACCACACGTGTAAGAAATAAGAGTATCATAAAACTAG  1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACCACACGTGTAAGAAATAAGAGTATCATAAAACTAG  1800

Qy   1801  TTCCATTTGGGGCCATCGTGTGTGTGTGCCATTCGTGTGTGTATAGGGGAGGAGGAGGCGCCCTGCAAGCACCCGGGTCC  1860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  TTCCATTTGGGGCCATCGTGTGTGTGTGCCATTCGTGTGTGTATAGGGGAGGAGGAGGCGCCCTGCAAGCACCCGGGTCC  1860

Qy   1861  TGAAGCCCCCGCAGAGGTTTCCTCTCCAGCTGCCCGTGCCACTCGGTTGTTTGTTATCACTCTCTAGG  1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  TGAAGCCCCCGCAGAGGTTTCCTCTCCAGCTGCCCGTGCCACTCGGTTGTTTGTTATCACTCTCTAGG  1920

Qy   1921  TGGGGTCCTGAGCAACCTGCTCTATTTCGTGTGACTCGTTCATTTCGTTGTTTGTTATCACTCTCATTGACAATT  1980
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  TGGGGTCCTGAGCAACCTGCTCTATTTCGTGTGACTCGTTCATTTCGTTGTTTGTTATCACTCTCATTGACAATT  1980

Qy   1981  GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCTATTTCTGTGTGACTCGTTCATTCATTGACAATT  2040
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCTATTTCTGTGTGACTCGTTCATTCATTGACAATT  2040

Qy   2041  TATTGAGTACTTATATCTGCCAGACACCAGACAAAATGTGAGCAAAGCAGTCACTGC  2100
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Db   2041  TATTGAGTACTTATATCTGCCAGACACCAGACAAAATGTGAGCAAAGCAGTCACTGC  2100

Qy   2101  CCTACCTTCGTGGAGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA  2160
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Db   2101  CCTACCTTCGTGGAGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA  2160

Qy   2161  GCCAACTAAACCCAGTGCTGCTGAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC  2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  GCCAACTAAACCCAGTGCTGCTGAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC  2220

Qy   2221  AGCATCCCTTAACAGAGGCACCTCCTAGGCGCCCCTGCCTCCATCGTGCCCCGGAGG  2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  AGCATCCCTTAACAGAGGCACCTCCTAGGCGCCCCTGCCTCCATCGTGCCCCGGAGG  2280

Qy   2281  CCCCCAAGCCCGAGTCTTCCTCCTCCTCCTCCATCAGTCAGGCCTCACAGGCTCGGCCT  2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  CCCCCAAGCCCGAGTCTTCCTCCTCCTCCTCCATCAGTCAGGCCTCACAGGCTCGGCCT  2340

Qy   2341  GCCTGCTTCCGTGAATCGTCCTGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT  2400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  GCCTGCTTCCGTGAATCGTCCTGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT  2400

Qy   2401  CCAGAAAGGAAATGAGAGGGAAACTAGTCTAACGGAGAATCTGAGGGGGACAGTGTTTC  2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  CCAGAAAGGAAATGAGAGGGAAACTAGTCTAACGGAGAATCTGAGGGGGACAGTGTTTC  2460

Qy   2461  CTCAGAGGGAAAGGGCCTCGAGCGGGTGCTGAGGGGTGCTGAAAAGGGTGAAAAGGGGTGAAA  2520
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Db   2461  CTCAGAGGGAAAGGGCCTCGAGCGGGTGCTGAGGGGTGCTGAAAAGGGTGAAAAGGGGTGAA  2520

Qy   2521  TGGGGACGCTGGGGTCGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGGCAAGGCTGAA  2580
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Db   2521  TGGGGACGCTGGGGTCGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGGCAAGGCTGAA  2580

Qy   2581  GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGAGTTTTCCGTTGCTTCCTGTGAGC  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGAGTTTTCCGTTGCTTCCTGTGAGC  2640

Qy   2641  CTTTTTATCTTTCTTCTGCTTGGAGAGGAAGAAGTCTATTCATGAAGGATGCAGTTTC  2700
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Db   2641  CTTTTTATCTTTCTTCTGCTTGGAGAGGAAGAAGTCTATTCATGAAGGATGCAGTTTC  2700

Qy   2701  ATAAAGTCAGCTGTTAAAATTCAGGTGTGCATGGGTTTTCCTTCACGAGGCCTTTAT  2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  ATAAAGTCAGCTGTTAAAATTCAGGTGTGCATGGGTTTTCCTTCACGAGGCCTTTAT  2760

Qy   2761  TTAATGGAATATAGGAAGGCAGCTCATTTCCTAGGCCGTTAATTCACGGAGAAGTGAC  2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  TTAATGGAATATAGGAAGGCAGCTCATTTCCTAGGCCGTTAATTCACGGAGAAGTGAC  2820

Qy   2821  TGGAGTCTTTTCTTCTTTCTTCATGTCTTCATGTCTTCTGGGCAACTACTACCCGTGCGTGGACTTGGCTTA  2880
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  TGGAGTCTTTTCTTCTTTCTTCATGTCTTCATGTCTTCTGGGCAACTACTACCCGTGCGTGGACTTGGCTTA  2880

Qy   2881  TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTCTTTCTTCTGGTTCTGTTCTGCCATT  2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTCTTTCTTCTGGTTCTGTTCTGCCATT  2940

Qy   2941  GGTTGGCTGTGCGACCCTTGCGACCGTGCAAGTGTCTCTCCCTCGGCCATAGTCTTCTCTGCT  3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  GGTTGGCTGTGCGACCCTTGCGACCGTGCAAGTGTCTCTCCCTCGGCCATAGTCTTCTCTGCT  3000

Qy   3001  ATAAAGACCCTTGCGAGCTTCGTGTTCTCGTTTGTTGTGAACACTTCCCTCGTGTGAGGGG  3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  ATAAAGACCCTTGCGAGCTTCGTGTTCTCGTTTGTTGTGAACACTTCCCTCGTGTGAGGGG  3060

Qy   3061  GGATGTTGAGGAGGGAAGGGAAGGAGGCAGCTGAGCCACAGGGAGGTGAGGG  3120
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Db   3061  GGATGTTGAGGAGGGAAGGGAAGGAGGCAGCTGAGCCACAGGGAGGTGAGGG  3120

Qy   3121  GGACACGGAAGCAGCAGAGAGCTGGTGCTCCATCAGTGCTCACTGATCACGTCAGACTC  3180
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Db  3121 GGACAGGAAGGCAGGCAGCAGAAGCTCGGGTGCTCCATCAGTCCTCACTCAGTCACGTCAGACTC 3180

Qy  3181 CAGGACCGAGAGCCACCAATGTCTTCAGGAAGAAGCTCAATGAACCCACAGCCACATTTTCCT 3240
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Db  3181 CAGGACCGAGAGCCACCAATGTCTTCAGGAAGAAGCTCAATGAACCCACAGCCACATTTTCCT 3240

Qy  3241 TCCCTAAGCATAGACAATGCATTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
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Db  3241 TCCCTAAGCATAGACAATGCATTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300

Qy  3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGAAAATGCCAGAGATTG 3360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGAAAATGCCAGAGATTG 3360

Qy  3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420

Qy  3421 AGTGACCTGCAGGCGCAGGGGAGGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
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Db  3421 AGTGACCTGCAGGCGCAGGGGAGGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480

Qy  3481 ACAGATTCATTCAAGGGCAGTGGAATTGACCACCAGGATTATAGTCCACGTGATCGTGG 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 ACAGATTCATTCAAGGGCAGTGGAATTGACCACCAGGATTATAGTCCACGTGATCCTGG 3540

Qy  3541 GTTCTAGGAGGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600

Qy  3601 CCTGATTTTCTAATACTATATTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAG 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 CCTGATTTTCTAATACTATATTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAG 3660

Qy  3661 GTAGTAACTGAGCGTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTTTTCTCTGT 3720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GTAGTAACTGAGCGTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTTTTCTCTGT 3720

Qy  3721 GGAGTTAGCAGCACAAGGGCAATCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 GGAGTTAGCAGCACAAGGGCAATCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780

Qy  3781 TAAAGCCAAAACAGATTCAAGCCTAGGTCTTGACTATATGATTGGTTTTTTGAAAAAT 3840
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Db  3781 TAAAGCCAAAACAGATTCAAGCCTAGGTCTTGACTATATGATTGGTTTTTTGAAAAAT 3840

Qy  3841 CATTTCAGCGATGTTTACTTCACAAGTATTGACACTGTGTTGGTATTAACACATAAAG 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 CATTTCAGCGATGTTTACTTCACAAGTATTGACACTGTGTTGGTATTAACACATAAAG 3900

Qy  3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGACTTAACTGCAGAAACCAATCAAA- 3959
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAAACCAATCAAT 3960

Qy  3960 AAGAATAGAATCTTAGAGCAAACTGTGTTCTCCAATCTGGAGGTGAGTCTGCCAGGG 4019
         ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db  3961 AAGAATAGAATCTTAGAGCAAACTGTGTTCTCCAC-TCTCGGAGGTGAGTCTGCCAGGG 4019

Qy  4020 CAGTTTGAAATATTTACTTCACAAGTATTGACACTGTGTTGGTATTAACAACATAAAG 4079
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Db  4020 CAGTTTGAAATATTTACTTCACAAGTATTGACACTGTGTTGGTATTAACAACATAAAG 4079

Qy  4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
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Db  4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139

Qy  4140 TTTATTGGCTATTGCCATTTGCTTTTGCTTTTTGTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
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Db  4140 TTTATTGGCTATTGCCATTTGCTTTTGCTTTTTGTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199

Qy  4200 GGGATTATTAACCTACAGTCCCAGAAAGCCTGTGAATTGAATTGAAATGAGGAAAAATTACATTT 4259
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db  4200 GGGATTATTAACCTACAGTCCCAGAAAGCCTGTGAATTGAATTGAAATGAGGAAAAAATTACGTTTT 4259
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Qy  4260 TTGTTTTTACCACCTTCTACTAACTAAATTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
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Db  4260 TTATTTTTACCACCTTCTACTAACTAAATTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319

Qy  4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTGTCATTACCAATAGAAATCACAGACAT 4379
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Db  4320 ACTCAAAGTGGTATAAGAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379

Qy  4380 TTTATACTATATTACACAGTTGTTGTTGCAGATACGTGTAAGTGAAGTATTTATACTCAAAACT 4439
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Db  4380 TTTATACTATATTACACAGTTGTTGTTGCAGGTACGTGTAAGTGAAATATTTATACTCAAAACT 4439

Qy  4440 ACTTTGAAATTAGACCTCCTGCTGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
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Db  4440 ACTTTGAAATTAGACCTCCTGCTGATCTTGTTTTTAACATATTAATAATAAAACATGTTTAA 4499

Qy  4500 AATTTGATATTTTGATAATCATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
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Qy  4560 TATATATTTGAAAACATCTTTCTGAGAGAGTTCCCCAGATTCACCAATGAGGTTCTTG 4619
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Db  4560 TATATATTTGAAAACATCTTTCTGAGAGAGTTCCCCAGATTCACCAATGAGGTTCTTG 4619

Qy  4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGGTGTGCTGAG 4679
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Db  4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGGTGTGCTGAG 4679

Qy  4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTGTTTAAAGCTAGGGGT 4739
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTGTTTAAAGCTAGGGGT 4739

Qy  4740 GAGGGGGAAATCTGCCGCTTCATAGGAATGCTCCCTGGTACGCTGGTGCTGT 4799
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4740 GAGGGGGAAATCTGCCGCTTCATAGGAATGCTCCCTGGTACGCTGGTGCTGT 4799

Qy  4800 CCTTGTGTTCTCGGCTGGCTGTTATTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4800 CCTTGTGTTCTCGGCTGGCTGTTATTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859

Qy  4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCGTTCCAATGAGTTTGCAGA 4919
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Db  4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCGTTCCAATGAGTTTGCAGA 4919

Qy  4920 GTGAATGGAAATATAAACTAGAAATAAATCAGCAGTAGTCCTG 4979
         |||||||||||||||||||||||||||||||||||||||||||
Db  4920 GTGAATGGAAATATAAACTAGAAATAAATCAGCAGTAGTCCTG 4979

Qy  4980 GTGTAAGTGTGTGTAC----GTGTGTGTGTG 5035
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Db  4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGG 5039

Qy  5036 AGATATAGGAACTATTATTGGGGTGCATAAATTGGGATTGTCTTTTTAAAAAGA 5095
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Db  5040 AGATATAGGAACTATTATTGGGGTGCATAAATTGGGATTGTCTTTTTTAAAAAGA 5099

Qy  5096 AACTCCAAAACAGACTTCGGAAGGTTATTTTCTAAGAATCTTGCTGGCGTGAAGGCA 5155
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Db  5100 AACTCCAAAACAGACTTCGGAAGGTTATTTTCTAAGAATCTTGCTGGCGTGAAGGCA 5159

Qy  5156 ACCCCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCGTCTTCCCCATGGAG 5215
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Db  5160 ACCCCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCGTCTTCCCCATGAGCCAGCAAGG 5219

Qy  5216 GGCTGGCTCCCCAGTATATAAACCTCTGGGCATGAGCCAGCAAGG 5271
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Db  5220 GGCTGGCTCCCCAGTATATAAACCTCTCGGAGCTCGGGCATGAGCCAGCAAGG 5275
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RESULT 8
US-10-509-595-1
; Sequence 1, Application US/10509595

; Publication No. US2005017O353A1
; GENERAL INFORMATION:
;   APPLICANT: Sysmex Corporation
;   APPLICANT: ASANO, Kaoru
;   APPLICANT: TAKAHATA, Takayuki
;   APPLICANT: NUMADA, Shigehiro
;   APPLICANT: MASAGO, Akinori
;   APPLICANT: KOUCHI, Yasuhiro
;   TITLE OF INVENTION: GENE EXAMINATION METHOD FOR JUDGING THE ONSET RISK OF GLAUCOMA
;   FILE REFERENCE: Q83447
;   CURRENT APPLICATION NUMBER: US/10/509,595
;   CURRENT FILING DATE: 2004-09-29
;   PRIOR APPLICATION NUMBER: JP 2002-093443
;   PRIOR APPLICATION FILING DATE: 2002-03-29
;   PRIOR APPLICATION NUMBER: PCT/JP03/03307
;   PRIOR APPLICATION FILING DATE: 2003-03-19
;   NUMBER OF SEQ ID NOS: 27
;   SOFTWARE: Patentin version 3.3
;
; SEQ ID NO 1
;   LENGTH: 6000
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-509-595-1

Query Match   76.2%;   Score 4017.4;   DB 9;   Length 6000;
Best Local Similarity   99.9%;   Pred. No. 0;
Matches 4052;   Conservative   0;   Mismatches   0;   Indels   1;   Gaps   3;

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Qy   1216 GCTCCACAGGAAGTCTCCCCACTCTGAGACTTCTGCATCACGATGTTACAGCCAGAGCTC 1275
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Db      1 GCTCCACAGGAAGTCTCCCCACTCTGAGACTTCTGCATCACGATGTTACAGCCAGAGCTC   60

Qy   1276 CGTGAGGGTGAGGGTCGTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGC 1335
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Qy   1336 AACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACT 1395
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Db    121 AACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACT  180

Qy   1396 ACAGGGCCACGCCGCCGGCTAATTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAG 1455
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Db    181 ACAGGGCCACGCCGCCGGCTAATTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAG  240

Qy   1456 CCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGC 1515
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Db    241 CCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGC  300

Qy   1516 TGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGTCAGTGTTTAATAAGGAATTAAC 1575
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Db    301 TGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGTCAGTGTTTAATAAGGAATTAAC  360

Qy   1576 TTGAATGGTTTACTAAACCAACCAACAGAGGAAAACAGACAAAAGCTGTAATTTGATAATTC 1635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1636 TTGGGATGGGGAATGGTGCCATGAGCTTGCCTGCCTAGTCCCAGACCACTGGTCCTCATCA 1695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TTGGGATGGGGAATGGTGCCATGAGCTTGCCTGCCTAGTCCCAGACCACTGGTCCTCATCA  480

Qy   1696 CTTTCTTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATTCACCATGCTTTTGTG 1755
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Db    481 CTTTCTTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATTCACCATGCTTTTGTG  540

Qy   1756 GTAAGCCTCACACATGTTACTGAGAATAAGAGTATATACATAAACTAGTTCCATTTGGGCCA 1815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTAAGCCTCCACACATGTTACTGAGAATAAGAGTATATACATAAACTAGTTCCATTTGGGCCA  600

Qy   1816 TCTGTGTGTATAGGGGAGGGGCATACCCCAGAGACTCCTTGAAGCCCCCGGCGCGAG 1875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TCTGTGTGTATAGGGGAGGGGCATACCCCAGAGACTCCTTGAAGCCCCCGGCGCGAG  660

Qy   1876 AGGTTCCTCTCCAGCTGGGGGAGCCCTGCCAAGCACCGGGGTCCTCGGGTGTCCTGAGCA 1935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGGTTCCTCTCCAGCTGGGGGAGCCCTGCCAAGCACCGGGGTCCTCGGGTGTCCTGAGCA  720

Qy   1936 ACCTGCCAGCCGTGCCACTGGTTCGTTCGTTGTTGTTATCACTCCTGGGGGACCTGTTGCTTTCT 1995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ACCTGCCAGCCGTGCCACTGGTTCGTTCGTTGTTGTTATCACTCCTGGGGGACCTGTTGCTTTCT  780

Qy   1996 ATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATTTATTGAGTACTTATA 2055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATTTATTGAGTACTTATA  840

Qy   2056 TCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGCCCTACCTTCGTGGAG 2115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGCCCTACCTTCGTGGAG  900

Qy   2116 GTGACAGTTTCTCATGAAGACGTGCAGAGAAATTAATAGCCAGCCAACTTAAACCCA 2175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GTGACAGTTTCTCATGAAGACGTGCAGAGAAATTAATAGCCAGCCAACTTAAACCCA  960

Qy   2176 GTGCTGAAAGAAAGAAATAAACACCATCTTGAAGAATTGTGCGCAGCATCCCTTAACAA 2235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GTGCTGAAAGAAAGAAATAAACACCATCTTGAAGAATTGTGCGCAGCATCCCTTAACAA 1020

Qy   2236 GGCCACCTCCCTAGCGCCCCCTGCGCCTCCTCCATCAGTCACAGCGCTGCAGCCGCTGGGGAGT 2295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGCCACCTCCCTAGCGCCCCCTGCGCCTCCTCCATCAGTCACAGCGCTGCAGCCGCTGGGGAGT 1080

Qy   2296 CTTCCAAGCCTCCTCCTCCTCTCCTCCATCGACGCTGCAGCTGGCCTGCCTGCCTTCCCGTG 2355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CTTCCAAGCCTCCTCCTCCTCTCCTCCATCGACGCTGCAGCTGGCCTGCCTGCCTTCCCGTG 1140

Qy   2356 AATCGTCCTGGTGCATCGAGGTCGCATCTGAGCTGGAGAATCTGGCTCCAGGCTCCAGGAAATGG 2415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AATCGTCCTGGTGCATCGAGGTCGCATCTGAGCTGGAGAATCTGGCTCCAGGCTCCAGGAAATGG 1200

Qy   2416 AGAGGGAAACTAGTCAACGGACAGTGTTCTCAGAGGGAAAGGG 2475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AGAGGGAAACTAGTCAACGGACAGTGTTCTCAGAGGGAAAGGG 1260

Qy   2476 GCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGGGACTGGGGC 2535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGGGACTGGGGC 1320

Qy   2536 TGAGCGGGTGCTGAAAGGCAGGAAGCTGAAAGGGCGAAGGCTGAAGCTGCCCAGATGTTC 2595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 TGAGCGGGTGCTGAAAGGCAGGAAGCTGAAAGGGCGAAGGCTGAAGCTGCCCAGATGTTC 1380

Qy   2596 AGTGTTGTTCACGGGGCTGGGAGTTTCCGTTGCTTCCGTTGCTTGTGAGCCTTTTATCTTTTCT 2655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AGTGTTGTTCACGGGGCTGGGAGTTTCCGTTGCTTCCGTTGCTTGTGAGCCTTTTATCTTTTCT 1440

Qy   2656 CTGCTTGGAGGAAGAAGTCTATTCATGAAGGGATGCAGTTTCATAAAGTCAGCTGTT 2715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CTGCTTGGAGGAAGAAGTCTATTCATGAAGGGATGCAGTTTCATAAAGTCAGCTGTT 1500

Qy   2716 AAAATTCCAGGGTGTGCATGGGGTTTCCTTCACGAAGGCCTTTATTTAATGGAATATAG 2775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AAAATTCCAGGGTGTGCATGGGGTTTCCTTCACGAAGGCCTTTATTTAATGGAATATAG 1560

Qy   2776 GAAGCGAGCTCATTTCCTAGGCTAAGTTAATTCACGGAGGAAGTGACTGGAGTCTTTTCTTT 2835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GAAGCGAGCTCATTTCCTAGGCTAAGTTAATTCACGGAGGAAGTGACTGGAGTCTTTTCTTT 1620

Qy   2836 CATGTCTTCTGGGCAACTACTCAGCCTGTGGTGGACTTGGCTTATGCGAAGACGTCGAA 2895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CATGTCTTCTGGGCAACTACTCAGCCTGTGGTGGACTTGGCTTATGCGAAGACGTCGAA 1680

Qy   2896 AACCTTGAATCAGGAGACTCGTTTTCTTTGTGGTCTGCCATTGGTTGGCGTGCGCGAC 2955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 AACCTTGAATCAGGAGACTCGTTTTCTTTGTGGTCTGCCATTGGTTGGCGTGCGCGAC 1740

Qy   2956 CGTGGGCAAGTGTCTCCTCCCTGCGAGACCCGGGGTCCTCGGGTGTCCTGAGCA 3015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CGTGGGCAAGTGTCTCCTCCCTGCGAGACCCGGGGTCCTCGGGTGTCCTGAGCA 1935
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Db  1741 CGTGGGCAAGTGTCTCTCCCTTCCCCTGGGCCATAGTCTTCTCTGCTATAAAGACCCTTGCA 1800

Qy  3016 GCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCCTCTGTGAGGGGGATGTTGAGAGGGG 3075
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 GCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCCTCTGTGAGGGGGATGTTGAGAGGGG 1860

Qy  3076 AAGGAGGCAGAGCTGGAGCAGTGAGCCAGCAGAGGGAGGTGGAGAGGTGAGAGGAAGGCAGG 3135
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 AAGGAGGCAGAGCTGGAGCAGTGAGCCAGCAGAGGGAGGTGGAGAGGTGAGAGGAAGGCAGG 1920

Qy  3136 CAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCAGTCCAGAGACCGAGAGCCA 3195
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 CAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCAGTCCAGAGACCGAGAGCCA 1980

Qy  3196 CAATGCTTCAGGAAAGCTCAATGAACCCACACAGCCACATTTCCTTCCCTAAGCATAGAC 3255
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CAATGCTTCAGGAAAGCTCAATGAACCCACACAGCCACATTTCCTTCCCTAAGCATAGAC 2040

Qy  3256 AATGGCATTTGCCAATAACCAAAAAGAATGCAGAGCTAACTGGTGGTAGCTTTTGCCTG 3315
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Db  2041 AATGGCATTTGCCAATAACCAAAAAGAATGCAGAGCTAACTGGTGGTAGCTTTTGCCTG 2100

Qy  3316 GCATTCAAAAACTGGGCCAGAGCAAGTGAAAATGCCAGAGATTGTTAAACTTTTCACCC 3375
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Db  2101 GCATTCAAAAACTGGGCCAGAGCAAGTGAAAATGCCAGAGATTGTTAAACTTTTCACCC 2160

Qy  3376 TGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCGACCGGAGTGACCTGCAGCGC 3435
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 TGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCGACCGGAGTGACCTGCAGCGC 2220

Qy  3436 AGGGGAGGAGAAGAGAAAGAGATGCGAGAGACTAGTGTATGAGCAAGAAAGACAGATTCATTCAAG 3495
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 AGGGGAGGAGAAGAGAAAGAGATGCGAGAGACTAGTGTATGAGCAAGAAAGACAGATTCATTCAAG 2280

Qy  3496 GGCAGTGGGAATTGACCACCAGGGGATTATAGTCCACGTGAAATCTTTTTCTCTGGGTTCTAGGAGGAGG 3555
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 GGCAGTGGGAATTGACCACCAGGGGATTATAGTCCACGTGAAATCTTTTTCTCTGGGTTCTAGGAGGCAGG 2340

Qy  3556 GCTATATTGTGGGGGGAAAAAATCAGTTCAAGGAGAAGTTCGGGAGACCTGATTTCTAATAC 3615
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 GCTATATTGTGGGGGGAAAAAATCAGTTCAAGGAGAAGTTCGGGAGACCTGATTTCTAATAC 2400

Qy  3616 TATATTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAGAGGTAGTAACTGAGGCT 3675
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 TATATTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAGAGGTAGTAACTGAGGCT 2460

Qy  3676 GTAAGATTACTTAGTTTCTCCTTATTAGGAACATTCCTAAGAGTAAAGCCAAACAGAT 3735
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 GTAAGATTACTTAGTTTCTCCTTATTAGGAACATTCCTAAGAGTAAAGCCAAACAGAT 2520

Qy  3736 AGGGCAATCCCGTTCTTTCTTTTAACAGGAGAAAACATTCCTAAGAGTAAAGCCAAACAGAT 3795
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 AGGGCAATCCCGTTCTTTCTTTTAACAGGAGAAAACATTCCTAAGAGTAAAGCCAAACAGAT 2580

Qy  3796 TCAAGCCTAGGTCTTGCTTGGACTATATGATTGGTTTTTTGAAAAATCATTTCAGGCGATGTT 3855
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 TCAAGCCTAGGTCTTGCTTGGACTATATGATTGGTTTTTTGAAAAATCATTTCAGGCGATGTT 2640

Qy  3856 TACTATCTGATTCAGAAAATGAGACTAGTAGCCCTTTGCTCAGCTGTAAACAACACCCAG 3915
         ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db  2641 TACTATCTGATTCAGAAAATGAGACTAGTAGCCCTTTGCTCAGCTGTAAACAACAACACCCAT 2700

Qy  3916 TTGTAAATGTCTCAAGTTCTCCAAGTTCAGCGTTAACTGCAGAACCAATCAAA-AAGAATAGAATCTTT 3974
         |||||||||||||||||    ||||||||||||||||||||||||||||||  |||||||||||||||
Db  2701 TTTGTAAATGTCTCAAGTTCTCAGCGTTAACTGCAGAACCAATCAAATAAGAATAGAATCTTT 2760

Qy  3975 AGAGCAAACTGTGTTTCTTCCCACATCTCGGAGGTGAGCTCGCCAGGGCAGTTTGGAAATATT 4034
         |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  2761 AGAGCAAACTGTGTTTCTTCCCAC-TCTCGGAGTGTGAGCTCGCCAGGGCAGTTTGGAAATATT 2819

Qy  4035 TACTTCACAAGTATTGACACTCGTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAGGCAAT 4094
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2820 TACTTCACAAGTATTGACACTCGTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAGGCAAT 2879
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Qy  4095 CATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTGTTATTGGCTATTGC 4154
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2880 CATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTGTTATTGGCTATTGC 2939

Qy  4155 CATTTGCTTTTTGTTTTTCTCTTTGGGTTATTAATGTAAAGCAGGGATTATTAACCTA 4214
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2940 CATTTGCTTTTTGTTTTTCTCTTTGGGTTATTAATGTAAAGCAGGGATTATTAACCTA 2999

Qy  4215 CAGTCCAGAAAGCCTGTGAATTGAATGAGGAAAAAATTACATTTTTGTTTTACCACCT 4274
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3000 CAGTCCAGAAAGCCTGTGAATTGAATGAGGAAAAAATTACATTTTTGTTTTACCACCT 3059

Qy  4275 TCTAACTAAATTTAACATTTATTCATTGCGAATAGAGCCATAAACTCAAAGTGGTAAT 4334
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3060 TCTAACTAAATTTAACATTTATTCATTGCGAATAGAGCCATAAACTCAAAGTGGTAAT 3119

Qy  4335 AACAGTACCTGTGATTTGTCATTACCAATAGAAATCACAGACATTTATACTATATTAC 4394
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3120 AACAGTACCTGTGATTTGTCATTACCAATAGAAATCACAGACATTTATACTATATTAC 3179

Qy  4395 AGTTGTTGCAGATACGTGTAAGTGAAAATATTATACTCAAAACTACTTTGAAATTAGAC 4454
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Db  3180 AGTTGTTGCAGATACGTGTAAGTGAAAATATTATACTCAAAACTACTTTGAAATTAGAC 3239

Qy  4455 CTCCTGCTGCATCGTGTTTTAACATATTAATAAAAACATGTTAAAATTTTGATATTTTG 4514
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3240 CTCCTGCTGCATCGTGTTTTAACATATTAATAAAAACATGTTAAAATTTTGATATTTTG 3299

Qy  4515 ATAATCATATTTCATTATCATTTGTTCCTTGTAATCTATATTTTATATATTTGAAAAC 4574
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3300 ATAATCATATTTCATTATCATTTGTTCCTTGTAATCTATATTTTATATATTTGAAAAC 3359

Qy  4575 ATCTTTCTGAGAAGAGTTCCCCAGATTCACCAATGAGGTTCTTGGCATGCATGCACACACA 4634
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3360 ATCTTTCTGAGAAGAGTTCCCCAGATTCACCAATGAGGTTCTTGGCATGCATGCACACACA 3419

Qy  4635 GAGTAAGAACTGATTTAGAGCTAACATTGGTGTGCCTGAGATGCAAGACTGAAAT 4694
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3420 GAGTAAGAACTGATTTAGAGCTAACATTGGTGTGCCTGAGATGCAAGACTGAAAT 3479

Qy  4695 TAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGGTGAGGGGTGAGGGGAAATCTG 4754
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3480 TAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGGTGAGGGGTGAGGGGAAATCTG 3539

Qy  4755 CCGCTTCTATAGGAAATGCTCTCCCCTGGGTGCTGTGTTCCTTGTCTGGCT 4814
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3540 CCGCTTCTATAGGAAATGCTCTCCCCTGGGTGCTGTGTTCCTTGTCTGGCT 3599

Qy  4815 GGCTGTGTTATTTTCTCTGTCCCCTGCTACGTCTTAAAGGACTTGTTGGATCTCCAGTTCC 4874
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3600 GGCTGTGTTATTTTCTCTGTCCCCTGCTACGTCTTAAAGGACTTGTTGGATCTCCAGTTCC 3659

Qy  4875 TAGCATAGTGCCTGGCACAGTTGCGCAGTTCTCAATGAGTTGCAGAGTGAATGGAAATATA 4934
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3660 TAGCATAGTGCCTGGCACAGTTGCGCAGTTCTCAATGAGTTGCAGAGTGAATGGAAATATA 3719

Qy  4935 AACTAGAAATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGTGTA 4994
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3720 AACTAGAAATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGTGTA 3779

Qy  4995 CGTGTGTGGTGCATAAATTGGGATGTTCTTTTTAAAAGAAACTCCAAACAGACTTCTG 5054
         | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3780 C--GTGTGTGGTGCATAAATTGGGATGTTCTTTTTAAAAGAAACTCCAAACAGACTTCTG 3837

Qy  5055 GGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAGAAACTCCAAACAGACTTCTG 5114
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Db  3838 GGGGTATGGTGCATAAATTGGGATGTTCTTTTTAAAAGAAACTCCAAACAGACTTCTG 3897

Qy  5115 GAAGGTTATTTTCTAAGAATCTTCTGCGCAGCGTGAAGCGTGAAGGCAACCCCCGTGCACAGCCC 5174
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3898 GAAGGTTATTTTCTAAGAATCTTCTGCGCAGCGTGAAGCGTGAAGGCAACCCCCGTGCACAGCCC 3957
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Qy    5175 CACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCATGAAGGGCTGCTCCCCAGTATAT 5234
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3958 CACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCATGAAGGGCTGCTCCCCAGTATAT 4017

Qy    5235 ATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAG 5271
           ||||||||||||||||||||||||||||||||||||
Db    4018 ATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAG 4054


RESULT 9
US-09-952-464A-1
; Sequence 1, Application US/09952464A
; Publication No. US20030077587A1
; GENERAL INFORMATION:
; APPLICANT: Stone, Edwin M.
; APPLICANT: Sheffield, Val C.
; APPLICANT: Alward, Wallace L.M.
; APPLICANT: Fingert, John
; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
; FILE REFERENCE: 21087.0017U11
; CURRENT APPLICATION NUMBER: US/09/952,464A
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/473,273
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 09/461,542
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 09/366,952
; PRIOR FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 09/056,285
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/822,999
; PRIOR FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. US20030077587A1e =
; OTHER INFORMATION: Synthetic construct
US-09-952-464A-1

Query Match        34.2%;  Score 1804.4;  DB 3;  Length 2800;
Best Local Similarity 99.8%;  Pred. No. 0;
Matches 1838;  Conservative 0;  Mismatches 1;  Indels 3;  Gaps 3;

Qy    3431 AGGCGCAGGGGAGGAGAGAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 3490
           ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1 AGGCGCAGGGGAGGAGAGAAAG-AAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 59

Qy    3491 TCAAGGGCAGTGGAATTGACCACCAGGAGGATTATAGTCCACGTGGTTCTAGGAG 3550
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      60 TCAAGGGCAGTGGAATTGACCACCAGGAGGATTATAGTCCACGTGGTTCTAGGAG 119

Qy    3551 GCAGGGCTATATTGTGGGGGGGAAAAAATCAGTTCAAGGGAGTCGGGAGGACCTGATTTCT 3610
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     120 GCAGGGCTATATTGTGGGGGGGAAAAAATCAGTTCAAGGGAGTCGGGAGGACCTGATTTCT 179

Qy    3611 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 3670
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Db     180 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 239

Qy    3671 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAGAACTCTTTTCTCCTGTGGAGTTAGCA 3730
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    3731 GCACAAGGGCAATCCCGTTTCTTTCTTTTAACAGAGAAAAACATTCCTAGAGAGTAAAGCCAAA 3790
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 GCACAAGGGCAATCCCGTTTCTTTCTTTTAACAGAGAAAAACATTCCTAGAGAGTAAAGCCAAA 359

Qy    3791 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTGAAAAATCATTTCAGCG 3850
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTGAAAAATCATTTCAGCG 419
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Db    3851 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTAGACTAGTACCCTTTGGT 3910
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     420 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTAGACTAGTACCCTTTGGT 479

Db    3911 CCCAGTTGTAAATGTCTCAAGTTCAGCTTCAGCTTCAGCGAGAACCAATCAAA-AAGAATAGAA 3969
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Qy     480 CCCATTTGTAAATGTCTCAAGTTCAGCTTCAGCTTCAGCGAGAACCAATCAAATAAAGAATAGAA 539

Db    3970 TCTTTAGAGCAAACTGTCTTCTCCACATCTGCGAGGTGAGTCTGCCAGGGCAGTTTGGAA 4029
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Qy     540 TCTTTAGAGCAAACTGTGTTCTCCAC-TCTGCGAGGTGAGTCTGCCAGGGCAGTTTGGAA 598

Db    4030 ATATTTACTTCACAAGTATTGACACTGTTGGTATTAACACATAAAGTTGCTCAAAG 4089
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     599 ATATTTACTTCACAAGTATTGACACTGTTGGTATTAACACATAAAGTTGCTCAAAG 658

Db    4090 GCAATCATTATTCAAGTGGCTAAAGTACTTCTGACAGTTTGTATATTTATTGGCT 4149
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     659 GCAATCATTATTCAAGTGGCTAAAGTACTTCTGACAGTTTGTATATTTATTGGCT 718

Db    4150 ATTGCCATTGCTTTGTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 4209
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     719 ATTGCCATTGCTTTGTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 778

Db    4210 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTGTTTTTAC 4269
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     779 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTGTTTTTAC 838

Db    4270 CACCTTCTAACTAAATTAACATTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 4329
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     839 CACCTTCTAACTAAATTAACATTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 898

Db    4330 GTAATAACAGTACCTGTGATTTGTCATTACCAATAGAAATCACAGATATTTATACTAT 4389
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     899 GTAATAACAGTACCTGTGATTTGTCATTACCAATAGAAATCACAGATATTTATACTAT 958

Db    4390 ATTACAGTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 4449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     959 ATTACAGTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 1018

Db    4450 TAGACCTTCCTGCTGGATCTTGTTTTAACATATTAATAAAACATGTTTAAAATTTGATA 4509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1019 TAGACCTTCCTGCTGGATCTTGTTTTAACATATTAATAAAACATGTTTAAAATTTGATA 1078

Db    4510 TTTTGATAATCATATTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 4569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1079 TTTTGATAATCATATTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 1138

Db    4570 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAGAGGTTCTGGCATGCACAC 4629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1139 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAGAGGTTCTGGCATGCACAC 1198

Db    4630 ACACAGATAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 4689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1199 ACACAGATAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 1258

Db    4690 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGA 4749
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1259 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGA 1318

Db    4750 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGTAGGGGTCGTTCCTTGTGTTC 4809
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1319 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGTAGGGGTCGTTCCTTGTGTTC 1378

Db    4810 TGGCTGCCTGTTATTTTTCTCTGTCCCTCGTCCTACGTCTTAAGGACTGTTTGGATCTCCA 4869
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1379 TGGCTGCCTGTTATTTTTCTCTGTCCCTCGTCCTACGTCTTAAGGACTGTTTGGATCTCCA 1438

Db    4870 GTTCCTAGCATAGTGCCTCGGCACAGTGCAGGTTCTCAATGAGTTGCAGAGTGAATGGAA 4929
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1439 GTTCCTAGCATAGTGCCTCGGCACAGTGCAGGTTCTCAATGAGTTGCAGAGTGAATGGAA 1498
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RESULT 10
US-10-017-870-10

; Sequence 10, Application US/10017870
; Publication No. US20030165857A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, DOUG HUI
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TIGR GENOTYPING ASSAYS
; FILE REFERENCE: 034827-1401
; CURRENT APPLICATION NUMBER: US/10/017,870
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-870-10

Query Match   34.2%; Score 1804.4; DB 6; Length 2800;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 1838; Conservative   0; Mismatches   1; Indels   3; Gaps   3;

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Db    300 GCACAAGGGCAATCCGTTCTTCTTTTAACAGAAGAAGAAACATTCCTAGAGTGAATGGAA 359

Qy   3791 CAGATTCAAGCCTAGTCTTGCTCAGTCAGTAGTCCTGGTGTAAGTGT 3850
               ||||||||||||||||||||||||||||||||||||||||||||||
Db    360 CAGATTCAAGCCTAGTCTTGCTGACTATATGATTGGTTTTTGAAAAATCATTTCAGCG 419

Qy   3851 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTGGTCAGCTGTAAACAAACA 3910
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTGGTCAGCTGTAAACAAACA 479

Qy   3911 CCCAGTGTAAATGTCTCAAGTCAGCTTAACTGCGTTAAAAGAAACTCCAAACAGAC 3969
               ||||||||||||||||||||||||||||||||  |||||||||||||
Db    480 CCCATTGTAAATGTCTCAAGTCAGCTTAACTGCGAGAAACAATCAAATAAGAATAGAA 539

Qy   3970 TCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGCGTGAGTCTGCGCCAGTTTGGAA 4029
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 TCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGCGTGAGTCTGCGCCAGTTTGGAA 598

Qy   4030 ATATTTACTTCACAAGTATTGACACTGTTGGTATTAACAACACATAAAGTTGCTCAAAG 4089
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    599 ATATTTACTTCACAAGTATTGACACTGTTGGTATTAACAACACATAAAGTTGCTCAAAG 658

Qy   4090 GCAATCATTATTTCAAGTGGCTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGCT 4149
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    659 GCAATCATTATTTCAAGTGGCTAAAGTTACTTCTGACAGTTTGGTATATTTATTGCT 718

Qy   4150 ATTGCCATTTGCTTTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGATTATTA 4209
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    719 ATTGCCATTTGCTTTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGATTATTA 778

Qy   4210 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAATTACATTTTGTTTTTAC 4269
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    779 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAATTACATTTTGTTTTTAC 838

Qy   4270 CACCTTCAACTAAATTAACATTTTATTCCATTGCCAATAGAGCCCATAAACTCAAAGTG 4329
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    839 CACCTTCAACTAAATTAACATTTTATTCCATTGCCAATAGAGCCCATAAACTCAAAGTG 898

Qy   4330 GTAATAACAGTACCTGTGATTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 4389
               ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    899 GTAATAACAGTACCTGTGATTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 958

Qy   4390 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTGAAAT 4449
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    959 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 1018

Qy   4450 TAGACCCTCCTGCTGGATCTTGTTTTTTAACATATTAATAATAAAACATGTTAAATTTGATA 4509
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1019 TAGACCCTCCTGCTGGATCTTGTTTTTTAACATATTAATAATAAAACATGTTAAATTTGATA 1078

Qy   4510 TTTTGATAATCATATTCATTATCATTGTTTCCTTTGTAATCTATATTTATATATTTG 4569
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1079 TTTTGATAATCATATTCATTATCATTGTTTCCTTTGTAATCTATATTTATATATTTG 1138

Qy   4570 AAAACATCTTTCTGAGAAGAGTTCCCCAGAGTTCACCCCAGATTCACCAATGAGGTTCTGGCACAC 4629
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1139 AAAACATCTTTCTGAGAAGAGTTCCCCAGAGTTCACCCCAGATTCACCAATGAGGTTCTGGCACAC 1198

Qy   4630 ACACAGATAAGAACTGATTTAGAGGCTAACATTGACATTGACCTGCCTGCAAGACT 4689
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1199 ACACAGATAAGAACTGATTTAGAGGCTAACATTGACATTGACCTGCCTGCAAGACT 1258

Qy   4690 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGAA 4749
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1259 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGAA 1318

Qy   4750 ATCTGCGCCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGCTCCTTGTGTTC 4809
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1319 ATCTGCGCCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGCTCCTTGTGTTC 1378

Qy   4810 TGGCTGCGTGTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGGATCTCCA 4869
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1379 TGGCTGCGTGTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGGATCTCCA 1438
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RESULT 11

US-10-278-698-294

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Qy   1439 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTGCAGAGTGAATGGAA 1498
Qy   4930 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACCAGTAGTCCTGGTGTAAGTGT 4989
Db   1499 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACCAGTAGTCCTGGTGTAAGTGT 1558

Qy   4990 GTGTAGCTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGAGATATAGGAGAACTA 5049
Db   1559 GTGTAGCTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGAGATATAGGAGAACTA 1618

Qy   5050 TTATTGGGGTATGGGTGCATAAATTGGGATGTCTTTTAAAAAGAAACTCCAAACAGAC 5109
Db   1619 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTAAAAAGAAACTCCAAACAGAC 1678

Qy   5110 TTCTGGAAGGTTATTTTCTAAGAATCTGCTGGCAGCGTGAAGGCAACCCCCTGTGCAC 5169
Db   1679 TTCTGGAAGGTTATTTTCTAAGAATCTGCTGGCAGCGTGAAGGCAACCCCCTGTGCAC 1738

Qy   5170 AGCCCCACCCAGCCTCACGTGCCACCTCTGTCCTCCCCATGAAGGGCTGGCTCCCCAG 5229
Db   1739 AGCCCCACCCAGCCTCACGTGCCACCTCTGTCCTCCCCATGAAGGGCTGGCTCCCCAG 1798

Qy   5230 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCCAAGG 5271
Db   1799 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCCAAGG 1840
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; Sequence 294, Application US/10278698
; Publication No. US2005003734A1
; GENERAL INFORMATION:
; APPLICANT: PathoArray GmbH
; APPLICANT: Stuhlmuller, Bruno
; APPLICANT: Haupl, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: O30027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 294
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-278-698-294

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Query Match       34.2%;    Score 1804.4;     DB 8;    Length 2800;
Best Local Similarity   99.8%;    Pred. No. 0;
Matches 1838;    Conservative   0;    Mismatches   0;    Indels   3;    Gaps   3;

Qy   3431 AGGCGCAGGGGAGGAGAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 3490
               ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db      1 ACGCGCAGGGGAGGAGAGAAG-AAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 59

Qy   3491 TCAAGGGCAGTGGAATTGACCACAGCAGGATTAGTCCACGTGATCCTGGGGTTCTAGGAG 3550
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 TCAAGGGCAGTGGAATTGACCACAGCAGGATTAGTCCACGTGATCCTGGGGTTCTAGGAG 119

Qy   3551 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAGGTCGGGAGACCTGATTTCT 3610
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAGGTCGGGAGACCTGATTTCT 179

Qy   3611 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACCAAGGTAGTAACTG 3670
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACCAAGGTAGTAACTG 239

Qy   3671 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGGAACTCTTTTTCTCTGTGTGAGTTAGCA 3730
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGGAACTCTTTTTCTCTGTGTGAGTTAGCA 299

Qy   3731 GCACAAGGGCAATCCGTTCTTCTTTTTAACAGAAGAAGAAACATTCCTAGAGTGAATGGCCAAA 3790
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   4870 GTTCCTAGCAGTAGTGCCTGGCACAGTGCAGTTCTCAATGAGTTTGCGAGAGTGAATGGAA 4929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1439 GTTCCTAGCAGTAGTGCCTGGCACAGTGCAGTTCTCAATGAGTTTGCGAGAGTGAATGGAA 1498

Qy   4930 ATATAAACTAGAAATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGTGTGTAAGTGT 4989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1499 ATATAAACTAGAAATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGTGTGTAAGTGT 1558

Qy   4990 GTGTACGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAGAACTA 5049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1559 GTGTACGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAGAACTA 1618

Qy   5050 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTAAAAGAAACTCCAAACAGAC 5109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1619 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTAAAAGAAACTCCAAACAGAC 1678

Qy   5110 TTCTTGGAAGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGCAACCCCCGTGTGCAC 5169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1679 TTCTTGGAAGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGCAACCCCCGTGTGCAC 1738

Qy   5170 AGCCCCACCCAGCCTCACGTGGCCACCCTCGTCTTCCCCCATGAAGGGCTGGCCTCCCAG 5229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1739 AGCCCCACCCAGCCTCACGTGGCCACCCTCGTCTTCCCCCATGAAGGGCTGGCCTCCCAG 1798

Qy   5230 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
          ||||||||||||||||||||||||||||||||||||||||||
Db   1799 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 1840
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RESULT 12
US-10-278-698-808
; Sequence 808, Application US/10278698
; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: PathoArray GmbH
; APPLICANT: Haupl, Thomas
; APPLICANT: Stuhlmuller, Bruno
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: 03002TUS
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 808
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-808

Query Match 34.2%;   Score 1804.4;   DB 8;   Length 2800;
Best Local Similarity 99.8%;   Pred. No. 0;
Matches 1838;   Conservative 0;   Mismatches 0;   Indels 3;   Gaps 3;

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Qy   3431 AGCGCAGGGAGGGAGGAGAAGAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGAGATTCAT 3490
          ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db      1 AGCGCAGGGAGGGAGGAGAAG-AAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGAGATTCAT 59

Qy   3491 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 3550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 119

Qy   3551 GCAGGGCTATATTGTGGGGGAAAAAATCAGTTCAAGGAGTCGGGAGACCTGATTTCT 3610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 GCAGGGCTATATTGTGGGGGAAAAAATCAGTTCAAGGAGTCGGGAGACCTGATTTCT 179

Qy   3611 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 3670
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 239

Qy   3671 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 3730
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 299

Qy   3731 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAGAAAACATTCCTAAGAGTAAAGCCAAA 3790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAGAAAACATTCCTAAGAGTAAAGCCAAA 359

Qy   3791 CAGATTCAAGCCTAGGTCTTGCTGCTAGTATATGATTGGTTTTTGAAAAATCATTTCAGCG 3850
          ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    360 CAGATTCAAGCCTAGGTCTTGCTGCTAGTATATGATTGGTTTTTGAAAAATCATTTCAGCG 419

Qy   3851 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTAGTACCCTTGGTCAGCTCGTAAACAAACA 3910
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTAGTACCCTTGGTCAGCTCGTAAACAAACA 479

Qy   3911 CCCAGTTGTAAATGTCTCAAGTTCAGCTTAACTGCAGAACCAATCAAA-AAGAATAGAA 3969
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db    480 CCCATTTGTAAATGTCTCAAGTTCAGCTTAACTGCAGAACCAATCAAATAAGAATAGAA 539

Qy   3970 TCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 4029
          ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    540 TCTTTAGAGCAAACTGTGTTTCTCCCAC-TCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 598

Qy   4030 ATATTTACTTCACAAGTAATTGACACTGTTGTGGTATTAACACTGTTTGCTCAAAG 4089
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    599 ATATTTACTTCACAAGTAATTGACACTGTTGTGGTATTAACACTGTTTGCTCAAAG 658

Qy   4090 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGCACAGTTTGGTATATTTATTGCT 4149
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    659 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGCACAGTTTGGTATATTTATTGCT 718

Qy   4150 ATTGCCATTTGCTTTTTGCTTTTTGTTTTTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 4209
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    719 ATTGCCATTTGCTTTTTGCTTTTTGTTTTTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 778

Qy   4210 ACCTACAGTCCAGAAAGCCTGTGAATTGAATGAGGAAAAAATTACATTTTTGTTTTAC 4269
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    779 ACCTACAGTCCAGAAAGCCTGTGAATTGAATGAGGAAAAAATTACATTTTTGTTTTTAC 838

Qy   4270 CACCTTCTAACTAAATTAACATTTTATTCATTGCAATAGAGCCATAAACTCAAAGTG 4329
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    839 CACCTTCTAACTAAATTAACATTTTATTCATTGCAATAGAGCCATAAACTCAAAGTG 898

Qy   4330 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAATCACAGACATTTTATACTAT 4389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    899 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAATCACAGACATTTTATACTAT 958

Qy   4390 ATTACAGTTGTTGCAGATACGTTGTAAGTCAAACATGTTTAAAATTTTGATA 4449
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    959 ATTACAGTTGTTGCAGATACGTTGTAAGTCAAACATGTTTAAAATTTTGAAAT 1018

Qy   4450 TAGACCTCCTGCTGCGATCTTGTTTTTAACATATTAAAAATGTTAAAATTTTGATA 4509
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1019 TAGACCTCCTGCTGCGATCTGGTTTTTAACATATTAAAAATGTTAAAATTTTGATA 1078

Qy   4510 TTTTTGATAATCATATTTCATTATCATTGTTTCCTTGTAATCATATTTTATATATTTG 4569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1079 TTTTTGATAATCATATTTCATTATCATTGTTTCCTTGTAATCTATATTTTATATATTTG 1138

Qy   4570 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTCACCGATGAGGTTCTTGGCATGCACAC 4629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1139 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTCACCGATGAGGTTCTTGGCATGCACAC 1198

Qy   4630 ACACAGTAAGAACTGATTTAGAGACTCAACATTGACATTGTGCCTGAGATGCAAGACT 4689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1199 ACACAGTAAGAACTGATTTAGAGACTCAACATTGACATTGTGCCTGAGATGCAAGACT 1258

Qy   4690 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGAA 4749
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1259 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 1318

Qy   4750 ATCTGCCGCTTCTATAGAATGCTTCTCCCCGGAGCCTGGTAGGGTGCGTCTGTTGTTC 4809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1319 ATCTGCCGCTTCTATAGAATGCTTCTCCCCGGAGCCTGGTAGGGTGCGTCTGTTGTTC 1378
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Qy  4810 TGGCTGGCTGTGTTATTTCTCTGTCCGCTACGTCTTAAAGGACTTGTTGGATCTCCA 4869
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1379 TGGCTGGCTGTGTTATTTCTCTGTCCCGCTACGTCTTAAAGGACTTGTTGGATCTCCA 1438

Qy  4870 GTTCCTAGCATAGTGCTGGCACAGTGCAGGTTCTCAATGAGTTGCAGAGTGAATGGAA 4929
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1439 GTTCCTAGCATAGTGCTGGCACAGTGCAGGTTCTCAATGAGTTGCAGAGTGAATGGAA 1498

Qy  4930 ATATAAACTAGAAATATATCCTGTTGAAATCAGCACCAGTAGTCCTGGTGTAAGTGT 4989
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1499 ATATAAACTAGAAATATATCCTGTTGAAATCAGCACCAGTAGTCCTGGTGTAAGTGT 1558

Qy  4990 GTGTACGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 5049
         ||||||||||||||||||||||||||||||       ||||||||||||||||||
Db  1559 GTGTACGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 1618

Qy  5050 TTATTGGGTATGGGTGCATAAATTGGGATGTTCTTTTAAAAAGAAACTCCAAACAGAC 5109
         |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
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RESULT 13
US-10-803-557-10
; Sequence 10, Application US/10803557
; Publication No. US20050095609A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, DOUG HUI
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TIGR GENOTYPING ASSAYS
; FILE REFERENCE: 034827-1401
; CURRENT APPLICATION NUMBER: US/10/803,557
; CURRENT FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: US/10/017,870
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-803-557-10

Query Match   34.2%; Score 1804.4; DB 9; Length 2800;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1838; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

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Qy  3551 GCAGGGCTATATGTGGGGGGGAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 3610
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Db   120 GCAGGGCTATATGTGGGGGGGAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 179

Qy  3611 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGACGCAAGGTCACACAGGTAACTG 3670
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGACGCAAGGTCACACAGGTAACTG 239
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1838; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

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Qy  3491 TCAAGGGCAGTGGGAATTGACCACCAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 3550
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Qy  3551 GCAGGGCTATATTGTGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGGTGTAAGTGT 3610
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Qy  3731 GCACAAGGGCAATCCCGTTCTTTAACAGGAGGAGAAAACATTCCTAAGAGTAAAGCCAAA 3790
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Db   659 GCAATCATTATTTCAAGTGGCTAAAGTTACTTCTGCAGTTTTGGTATATTATTGGCT 718

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Qy  4450 TAGACCTTCCTGCTTGGATCTTGTTTTAACATATTAATAAAAACATGTTTAAAATTTTGATA 4509
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Qy  4810 TGGCTTGGCTGTTATTTTCTGCTGCCCTGCTACGTCTTAAAGGACTTGTTGGATCTCCA 4869
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Db  1559 GTGTACGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGTGAGATATAGGAACTA 1618

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Db  1619 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTAAAAGAAACTCCAAACAGAC 1678

Qy  5110 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTCGGCAGCGTGAAGGCAACCCCCGTGTGCAC 5169
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Db   1079  TTTTGATAATCATATTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG  1138

Qy   4570  AAAACATCTTTCTGAGAAGAGTTCCCCAGATTCACCAATGAGGTTCTTGGCATGCACAC  4629
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Db      1  TGAGGGTCTGTCTTACACCTACCTGTATGCTCACCTGAGCTCACTGCAACCTCTG  60

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Db    121  ACGCCMGGCTAATTTTGTATTGTTAGTAGGATGGGGTTTCACCATTATTAGCCCGGCTG  180

Qy   1464  GTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCCTAAAGTGCCTCCTAAAGTGCTGGGATTA  1523
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Qy   1524  CAGGCATGAGTGAGTCACCCGCCCGGCAAACAGACAAAAGCTGTGATAATTTCAGGGATG  1583
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Qy   1584  TTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGATAATTTCAGGGATG  1643
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Qy   1644  GGGAATGGTGCCATGAGCTGCCTAGTCCCAGACCACTGGTCCTCATCACTTTCTC  1703
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Qy   1824  TGTGTATAGGGAGGAGGCATACCCCAGAGACTCCTTGAAGCCCCGGCAGAGGTTTCC  1883
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Db    541  TGTGTATAGGGAGGAGGCATACCCCAGAGACTCCTTGAAGCCCCGGCAGAGGTTTCC  600

Qy   1884  TCTCCAGCTGGGGAGCCCTGCAAGCACCCGG  1915
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Search completed: January 26, 2006, 10:09:05
Job time : 2632 secs

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    January 26, 2006, 04:13:16 ; Search time 514 Seconds
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                                        8518.386 Million cell updates/sec

Title:             US-09-227-881-34
Perfect score:     5271
Sequence:          1 atctttgttcagttacctc.......tcgggcatgagaccagcaagg 5271
Scoring table:     IDENTITY_NUC
                   Gapop 10.0 , Gapext.1.0
Searched:          6059551 seqs, 41533918 residues

Total number of hits satisfying chosen parameters:      12119102

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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       11: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1		190.8	3.6	16525	8	US-11-136-527-717	Sequence 717, App
2	c	185.4	3.5	86361	7	US-10-995-561-13364	Sequence 13364, A*
3		185.2	3.5	143389	8	US-11-112-908-30	Sequence 30, Appl
4		185.2	3.5	150314	8	US-11-112-908-24	Sequence 24, Appl
5		185.2	3.5	166020	8	US-11-112-908-28	Sequence 28, Appl
6	c	184		60754	7	US-10-995-561-13440	Sequence 13440, A
7		183.4	3.5	415117	7	US-10-995-561-13274	Sequence 13274, A
8		179.6	3.4	14804	7	US-10-995-561-13379	Sequence 13379, A
9	c	179.6	3.4	98716	7	US-10-995-561-13331	Sequence 13331, A
10		179.6	3.4	191091	8	US-11-121-086-60	Sequence 60, Appl
11	c	179	3.4	159497	8	US-11-112-908-61	Sequence 61, Appl
12	c	179	3.4	171427	8	US-11-112-908-60	Sequence 60, Appl
13	c	178.4	3.4	127917	7	US-10-775-169-82	Sequence 82, Appl
14		177.8	3.4	161994	8	US-11-112-908-57	Sequence 57, Appl
15		177.8	3.4	168656	8	US-11-112-908-59	Sequence 59, Appl
16		177.8	3.4	100285	8	US-11-112-908-58	Sequence 58, Appl
17	c	177.8	3.4	387780	7	US-10-995-561-13259	Sequence 13259, A
18		177.6	3.4	128978	7	US-10-775-169-345	Sequence 345, Appl
19	c	176.8	3.4	55332	5	US-10-786-065-3	Sequence 3, Appli
20		176.8	3.4	179777	8	US-11-121-086-106	Sequence 106, App
21	c	176.6	3.4	1154	8	US-11-145-703-37	Sequence 37, Appl
22		176.6	3.4	153142	8	US-11-121-086-27	Sequence 27, Appl

23	c	176.2	3.3	1301	8	US-11-145-703-36	Sequence 36, Appl
24	c	176.2	3.3	1386	8	US-11-145-703-40	Sequence 40, Appl
25		176	3.3	207600	8	US-11-112-908-31	Sequence 31, Appl
26	c	176	3.3	319608	8	US-11-145-703-1	Sequence 1, Appli
27		175.6	3.3	177623	8	US-11-112-908-41	Sequence 41, Appl
28		175	3.3	86081	7	US-10-995-561-13246	Sequence 13246, A
29		174.8	3.3	17455	7	US-10-995-561-13426	Sequence 13426, A
30	c	174.8	3.3	28724	7	US-10-995-561-13372	Sequence 13372, A
31	c	174.8	3.3	155989	8	US-11-121-086-57	Sequence 57, Appl
32	c	174.8	3.3	180654	8	US-11-121-086-58	Sequence 58, Appl
33	c	174.6	3.3	40987	7	US-10-995-561-13503	Sequence 13503, A
34		174.6	3.3	67088	7	US-10-995-561-13365	Sequence 13365, A
35	c	174.6	3.3	79528	7	US-10-276-233A-6	Sequence 6, Appli
36		174.4	3.3	60844	7	US-10-995-561-13359	Sequence 13359, A
37		174.2	3.3	115935	7	US-10-775-169-241	Sequence 241, App
38	c	174.2	3.3	141121	7	US-10-995-561-13262	Sequence 13262, A
39	c	174.2	3.3	162289	8	US-11-121-086-20	Sequence 20, Appl
40	c	174.2	3.3	191684	8	US-11-121-086-2	Sequence 2, Appli
41		174.2	3.3	197096	8	US-11-121-086-107	Sequence 107, App
42	c	174	3.3	13609	7	US-10-995-561-13442	Sequence 13442, A
43	c	174	3.3	16082	7	US-10-995-561-13485	Sequence 13485, A
44	c	174	3.3	23894	7	US-10-995-561-13320	Sequence 13320, A
45	c	174	3.3	87672	7	US-10-995-561-13237	Sequence 13237, A

ALIGNMENTS

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RESULT 1
US-11-136-527-717
; Sequence 717, Application US/1136527
; Publication No. US2005028757O0A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE:  2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 717
;   LENGTH: 16525
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-717

Query Match           3.6%;   Score 190.8;  DB 8;  Length 16525;
Best Local Similarity 55.9%;   Pred. No. 6.1e-33;
Matches  871;  Conservative  0;  Mismatches  542;  Indels 145;  Gaps  21;

Qy  2387  CTTGGCTCCAGGCTCCAGAAAGGAAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGA  2446
              |||||||||||||||||||||||||||||||||||||||  |||||| |||||||||
Db  2815  CCTGGCTCCTGGCTCCAGAAAGGATATGGAGATGGAAATAGTCTCCCTGAACATTTGGA  2874

Qy  2447  GGGGACAGTGTTTCCTCAGAGGGAAAGAGGGCCTCCACGTTCCAGAGAATTCCAGGAGGTG  2506
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db  2875  ATGGCCAGTGTTTCCTCAGTGGGAAAAGAGTCTCTGTGTCC---AGAAATCCAGGAGGTG  2931

Qy  2507  GGGACTGCAGGGAGTGGGGACGCTGGGCCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAA  2566
              |||||||||||||||||||||||| |||||      ||||||||||||||||||||||
Db  2932  GGGACTGCAGCAGGGAGGGCTGCTG------GCCTGCCAGGAGTGCACAGGAAGGTGAAA  2981

Qy  2567  AGGGCAAGCTGAAGCTGCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTCGGGAGTTTTCCGT  2626
              |||| |||||   |||| |||||||||||||||||||||||||||||||||||||||
Db  2982  AGGG-TAGGCTAAATCTCACCAGATGTTGTCGCCTGCTGTGGAGTAGGGAGGCCCTGT  3040

Qy  2627  TGCTTCCTGTGAGCCTTTTTATCTTTCTGCTTGAGGAGGAGAAGTCTATTTCATGA  2686
              |||||||||||| ||| ||||||||||||||||| |||||     ||||||||||
Db  3041  TTCTCCCACAGGGCC------CATTTCTGGGCTTAGAGGAGGAACGGTTCTATCTTATGA  3093
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Qy  2687 AGGGATGCAGTTTCATAAAGTCAGCTTGTTAAAATTCCAGGTGTGCATGGGTTTTTCCTTC 2746
              ||||||||||||||||||||||||      ||||||     ||||||||||||
Db  3094 AAGGATGCAGTTTCATTGTAACTCATTTGCTAAAAGTCAAGGTGCCGTAAGTTTTTCCGGC 3153

Qy  2747 ACGAAGGCCTTTATTTATTAATGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTC 2806
              |||||||||      ||||||   ||||||||||||||||||||||||   ------
Db  3154 ACTGAAGGCTTTCATTTACTG-----GGAAAGCAAGTTCATTTCCTAGCGCATTGGCTC 3208

Qy  2807 ACGGAAGAAGTGACTGGAGTCTTTTCTTCATGTCTTCGGCAACTACTCAGCCCTGTG 2866
              |||||||||||||||||||||||   ||||||||||      ||||||||||
Db  3209 ATGGGAGAAGTGACTGATGTGTCTCATGAC----TTTGTGGCAAAGTGGTGGGCAATTTC 3264

Qy  2867 GTGGACTTGGCTTATGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTT 2926
              ||||||||||||||||||||||||||||||      ----
Db  3265 TCTGACTTGGCTGACATGAAAAGGT--GAAGCCTGGATTCAGGA-----GGTGTTCCTT 3317

Qy  2927 CTGGTTCTGCCATT--GGTTGGCTGCGACCGTGGCAAGTGTCCTCTTCCTCCTCTTCTTT 2983
              |||||||||||||    |||||||||||||   ||||||||||||||||||||||
Db  3318 CTGGCCATGCTATTTAGCCTTGCTGTGTGACCCAGAGCAAGAATCTCTCTCCTTTTCCGG 3377

Qy  2984 CCATAGTCTTCTGCTATAAAGACCCTTGCAGCTCTCGTGTTCTGTGTTCTG--------- 3043
              ||||||||   |||||||||||||||||||   |||||||
Db  3378 GCTTTAGTTTTTGCTCAACTCGAAGGGCCCAGCCCCGGTGTTCTG-------------- 3423

Qy  3044 TGATTCCTGTGAGGGGGGATGTTGAGAGGAAGGAGCAGAGCTGGAGCAGCTGAGCC 3103
                      -----TATGTAGGAGAAGCTGAGAACTGTGTAGGAGGCTGGGCTCAATCA------CT 3469
Db  3424 ------TATGTAGGAGAAGCTGAGAACTGTGTAGGAGGCTGGGCTCAATCA------CT 3469

Qy  3104 ACAGGGGAGGTCGAGGGGGACAGGAGGCAGGCAGAGAAGCTCGGGTGCGTCCATCAGTCCTCA 3163
              ||||||||||||||||||||||||||||||||||||||||||||
Db  3470 GAGCGTGAAGAGGTGGCGTTGGTTGGTGAGCAGAGATGTGATGCTCATCAGTCCCTA 3529

Qy  3164 CTGATCACGTCAGACTCCAGGACCGAGACCCAGAAAGCTCAATGAACCC 3223
              ||.|||||||||||||||||||   ||||||||||||||||||
Db  3530 CCTGCCGTCCGAGGTGGGA-----GAGAGCCGGAGTCGACTGACTGAAGAAGCGGGGCTCAACAAC 3584

Qy  3224 AACAGCCACATTTCCTTCCCTAAGCATAGACACAATGGCATTTGCCAATAACCAAAAGAA 3283
              |||||||      ||||||||||||||||||||   ||||||||||||||||||
Db  3585 AAGAGAAATCCCTATCTTCTTTCCCCTAAGTCAT--GCATCTGCCCAGGAACTAGGAGAA 3643

Qy  3284 TGCAGAGACTAACTGGTGGTAGCTTTGCCTGGCATTCAAAAAACTGGGCCAGAGCAAGTG 3343
              |||||||||||||||||||||||||      |||||||||||||||||
Db  3644 AGCAGACAGTGACAGGTTG-----TCTGTGCTGGTATCTACAAATGGGGCTGGAGTGAGC 3699

Qy  3344 GAAAAATGCCAGAGATTGTAAACTTTCACCCTGACCAGCACCCGACCAGCTCAGCGAGT 3403
              |||||||   |||||||||   ||||||||   |||||||||||||||||||
Db  3700 GGAAATGCCAGGACCGGTTGTCCATTTCACCCTGGCCAGGATCCACAGCCGGCGACAAC 3759

Qy  3404 GACTGCTGACAGCACGGAGCTGACCTGAGCGAGAGGAGAGAAAGAGAGGGATA 3463
              -|||||||||||||||||||   |||||||||||||||||||
Db  3760 GGCTGCTGGTGTGGCAGACTAACCTGCAGGTTACAGGGGCGACGGTGAGG-- 3817

Qy  3464 GTGTATGAGCAAGAAGACAGATTCATTCAAGTGAATTGACCACCAGGGATTAT 3523
              |||||||||||||||||||||||||||   ||||||||||||||
Db  3818 ------------GAAAGAGACAGAGATCTACAAGGAGACTCACAAGCGCCCACTGACTGTGTAG 3861

Qy  3524 AGTCCACGTGATCTCGGGTTCTAGGAGGCAGGCAGCTAAATACTATATTTTCCTTTACAAGTCAGT 3583
              |||||||   ||||||      ||||||||||||
Db  3862 AGCACGGGCATGATGAGCCAAGCATGAAGGGTCCTAGCTGGGTCGTGTGCGTGTGGGGGAAGA 3918

Qy  3584 CAAGGGAAGTCGGGAGACCTGATTTCTAATACTATAATTTTCCTTTACAAGTCTGAGTAAT 3643
              ||||||   ||||||||||||||   ||||||||||||||||||
Db  3919 TGACTCAAGTCAGAAGCCCTA--CCCTAGTTCTGTGTTCTTCTTCAGAAGGCAAAGCAGC 3976

Qy  3644 TCTGAGCAAGTCACAAGGTAGTAACTGAGCGGCTGTAAGATTACTTAGTTGTTCTCCTTATTAG 3703
              |||||||||||||||      |||||||||||||||
Db  3977 CC-----------------CTCTTGCTTACATTCTC--TTTCCA 4001

Qy  3704 GAACTCTTTTTCTGTGGAGTTAGCAGCACAAGGGCAAATCCCGTTTCTTTTTAACAGGAA 3763
              |||||||      ||||||   |||||||||   |||
Db  4002 GAATTCTTTCTCACTACACAGCTGGCAGCAGGCAAGAATCAT--CTTGTTCCTTTCAAAAGAA 4059

Qy  3764 GAAAACATTCCTAAGAGTAAGCCAAACAGATTCAAGCTGACTGACTATATGA 3823
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RESULT 2

US-10-995-561-13364/c

; Sequence 13364, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13364
; LENGTH: 86361
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(86361)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables
US-10-995-561-13364

Query Match   3.5%; Score 185.4; DB 7; Length 86361;
Best Local Similarity 79.9%; Pred. No. 2e-31;
Matches 234; Conservative 0; Mismatches 51; Indels 8; Gaps 1;

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Qy  1290 TCTGTGTTCTTCACCTACCTGTATGCTCTACACCTGAGCTCTACACCTCTGCACCTGCCTCCC 1349
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 10562 TCTGTTGTCCTAGGCTGGAGTGCAGTGGCATGGACATCCTCAGCTTACTGCAACCTCTGCCTCCC 10503

Qy  1350 AGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGGGTAGCTGGGACTACAGCGCG-------- 1402
              AGGTTCAAGCGATTCTCCTGTCTCTGCCTCCCGGGTTGCTGGGACTATAGGCGTGTACCA 10443
Db 10502 AGGTTCAAGCGATTCTCCTGTCTCTGCCTCCCGGGTTGCTGGGACTATAGGCGTGTACCA 10443

Qy  1403 -CACGCCCGGCTAATTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCCGC 1461
              CCATGCCCGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATATTGGCTAGGC 10383
Db 10442 CCATGCCCGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATATTGGCTAGGC 10383

Qy  1462 TGGTCTTGAACTCCTGACCTCAGGTGATCCCACCCACCTGGCCTCCCAAAGTGCTGGGAT 1521
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 10382 TGGTCTTGAACTCCTGACCTCAGGTGATCCCGACCTCCAGGTCCCAAAGTGCTGGGAT 10323

Qy  1522 TACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTAATAAGGAATAA 1574
              ||||||||||||||||||||||||||||||||   ||||||||
Db 10322 TACAGGCATGAGCGAGCCACTGTGCCCGGCCAAAAATCTGGTATTTCAAATAAAAA 10270
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RESULT 3

US-11-112-908-30

; Sequence 30, Application US/11112908
; Publication No. US20050260655A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758

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Db  4060 AGAAATTTCCTAAGATATAGAGTATAGGCAAATAGATTTGAACCTCATTCCTGCTGACTATGGGA 4119
              ||||||||||||||||||||||||||||||||||||||||||||||
Qy  3824 TTGGTTTTTTGAAAATCATTTCAGCGATGTTACTATCTGATTCAGAAAATGAGACTAG 3883

Db  4120 TTGTTTTTTTAAAAAATCATTTTCAGTA------ATTCTGATTTACGAAAAGAGAACAG 4172
              ||||||||||||||||||||||||
Qy  3884 TACCCTTGGTCAGCTGAAACAAACACCAGTTGTAAATGTCTCAAGTTCAGGCTTA 3941

Db  4173 CACTTGCTTAGTCAGCAGTAAACAGGAAGCCGTTCTCTACGGTCCCCAGCCTCAGGGTTTA 4230
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; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30
; LENGTH: 143389
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-30

Query Match   3.5%;   Score 185.2; DB 8; Length 143389;
Best Local Similarity 79.4%; Pred. No. 2.7e-31;
Matches 235; Conservative   0; Mismatches 53; Indels   8; Gaps   1;

Qy   1280 AGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACC 1339
           || ||| | ||||| | |||||| |||||||||||||||||||||||||||| ||||||
Db 113274 AGAGTGTTGCTCGTGTCACCCAGATTGGAGTCAGTGGCACAATCTCAGCTCACCGCAACC 113333

Qy   1340 TCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCCAGCCTCCCGCGTAGTGTGGGACTACAG 1399
           |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db 113334 TCCGCCTCCCAGGTTCAAGCAATTCTCCTGCCTCCCGAGTAGGTGGGACTACAG 113393

Qy   1400 GCG-------CACGGCCCACCACCGCCTGGCTAATTTTGTATTGTTAGTAGAGATGGGGTTTCACCATA 1451
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 113394 GCGCCCGCCACCACGCCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATA 113453

Qy   1452 TTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCACCCTCAGCCTCCTAAA 1511
           |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db 113454 TTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGGCAATCCACCCACCCTCGGCCTCCCAAA 113513

Qy   1512 GTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAA 1567
           ||||||||||||||||||| ||||||||||||||||||||||||||||||||| |
Db 113514 GTGCTGGGATTACAGGTGTGAGCCACCGTGCCCGGCCTGTGCCCGGCCTGTTTTGACTCTTTTATGA 113569

RESULT 4
US-11-112-908-24
; Sequence 24, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
;   APPLICANT: Harris, Cole
;   APPLICANT: Davis, Lisa M.
;   TITLE OF INVENTION: Breast Cancer Biomarkers
;   FILE REFERENCE: 04-164-US
;   CURRENT APPLICATION NUMBER: US/11/112,908
;   CURRENT FILING DATE: 2005-04-22
;   PRIOR APPLICATION NUMBER: US 60/564,758
;   PRIOR FILING DATE: 2004-04-23
;   PRIOR APPLICATION NUMBER: US 60/575,978
;   PRIOR FILING DATE: 2004-06-01
;   PRIOR APPLICATION NUMBER: US 60/631,702
;   PRIOR FILING DATE: 2004-11-30
;   PRIOR APPLICATION NUMBER: US 60/633,826
;   PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 150314
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-24

Query Match   3.5%;   Score 185.2; DB 8; Length 150314;
Best Local Similarity 79.4%; Pred. No. 2.8e-31;
Matches 235; Conservative   0; Mismatches 53; Indels   8; Gaps   1;

Qy   1280 AGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACC 1339
           || ||| | ||||| | ||||| | |||||

Db 27741 AGAGTGTTGCTCGTGTCACCCAGATTGGAGTGCAGTGGCACAATCTCAGCTCACCGCAACC 27800

Qy 1340 TCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCCCGCGTAGTGTGGGACTACAG 1399
         |||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db 27801 TCCGCCTCCCAGGTTCAAGCAATTCTCCTGCCTCCCGAGTAGGTGGGACTACAG 27860

Qy 1400 GCG-------CACGGCCCACCACCGCCTGGCTAATTTTGTATTGTTAGTAGAGATGGGGTTTCACCATA 1451
         ||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 27861 GCGCCCGCCACCACGCCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATA 27920

Qy 1452 TTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCACCCTCAGCCTCCTAAA 1511
         |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db 27921 TTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGGCAATCCACCCACCCTCGGCCTCCCAAA 27980

Qy 1512 GTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAA 1567
         ||||||||||||||||||| ||||||||||||||||||||||||||||||||| |
Db 27981 GTGCTGGGATTACAGGTGTGAGCCACCGTGCCCGGCCTGTGCCCGGCCTGTTTTGACTCTTTTATGA 28036

RESULT 5
US-11-112-908-28
; Sequence 28, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
;   APPLICANT: Harris, Cole
;   APPLICANT: Davis, Lisa M.
;   TITLE OF INVENTION: Breast Cancer Biomarkers
;   FILE REFERENCE: 04-164-US
;   CURRENT APPLICATION NUMBER: US/11/112,908
;   CURRENT FILING DATE: 2005-04-22
;   PRIOR APPLICATION NUMBER: US 60/564,758
;   PRIOR FILING DATE: 2004-04-23
;   PRIOR APPLICATION NUMBER: US 60/575,978
;   PRIOR FILING DATE: 2004-06-01
;   PRIOR APPLICATION NUMBER: US 60/631,702
;   PRIOR FILING DATE: 2004-11-30
;   PRIOR APPLICATION NUMBER: US 60/633,826
;   PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 166020
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-28

Query Match   3.5%;   Score 185.2; DB 8; Length 166020;
Best Local Similarity 79.4%; Pred. No. 2.9e-31;
Matches 235; Conservative   0; Mismatches 53; Indels   8; Gaps   1;

Qy   1280 AGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACC 1339
           || ||| | ||||| | |||||| |||||||||||||||||||||||||||| ||||||
Db 159755 AGAGTGTTGCTCGTGTCTGTGTCTTCACCCAGATTGGAGTCAGTGGCACAATCTCAGCTCACCGCAACC 159814

Qy   1340 TCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCCAGCCTCCCGCGTAGTGTGGGACTACAG 1399
           |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db 159815 TCCGCCTCCCAGGTTCAAGCAATTCTCCTGCCTCCCGAGTAGGTGGGACTACAG 159874

Qy   1400 GCG-------CACGGCCCACCACCGCCTGGCTAATTTTGTATTGTTAGTAGAGATGGGGTTTCACCATA 1451
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 159875 GCGCCCGCCACCACGCCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATA 159934

Qy   1452 TTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCACCCTCAGCCTCCTAAA 1511
           |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db 159935 TTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGGCAATCCACCCACCCTCGGCCTCCCAAA 159994

Qy   1512 GTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAA 1567
           ||||||||||||||||||| ||||||||||||||||||||||||||||||||| |
Db 159995 GTGCTGGGATTACAGGTGTGAGCCACCGTGCCCGGCCTGTGCCCGGCCTGTTTTGACTCTTTTATGA 160050

RESULT 6
US-10-995-561-13440/c

Matches 241; Conservative 0; Mismatches 66; Indels 8; Gaps 1;

```
Qy    1280 AGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTTCACCTGAGCTCACTGCAACC 1339
           |||||  ||| || ||  |||    |||      |||      |||||||||||||||||
Db   60473 AGAGTCTTGCTCTGTCACCCGCTGTAGTGCAATGGCGCAATCTCAGCTCACTGCAACC 60532

Qy    1340 TCTGCCTCCCAGGTTCAAGCAATTCTCCGTCTCAGC    TGGGACTACAG 1399
           |  ||||||||||||||||| ||||||| | |||||    ||||| |||||
Db   60533 TCCGCCTCCCAGGTTCAAGTGATTCTCCTGCCTCAGCCTCTGAGTAGCTGGGATTACAG 60592

Qy    1400 GCG-------CACGCCGGCTAATTTGTTGTTAGTAGAGATGGGGTTTCACCATA 1451
           | |       | |||| |||||||| || | | |||||||||||||| | |||
Db   60593 GTGAGTGCACATGCCGCCGGCTAATTTTTTGTATTTTTAGTAGAGATGGGGTTTACCATG 60652

Qy    1452 TTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCACCCACCTCAGCCTCCTAAA 1511
           || ||| ||||||||| ||||||||   ||||||||||||  |||| ||| ||| |||
Db   60653 TTGGCCAGGCTGGTCTCGAACTCCTCAGGTGATCCAGCCACCACCTTGGCCTCCCAAA 60712

Qy    1512 GTGCTGGGATTACAGGCATGAGTCACCGCCGCCGGCCAAGGGTCAGTGTTAATAAGGAA 1571
           |||||||||||||||||  ||  |||| |||| ||||  | |     |||    |   |
Db   60713 GTGCTGGGATTACAGGCGTAAGCACCACCGCCTGGCCTAGGCCAAATAATTTTATGAAC 60772

Qy    1572 TAACTTGAATGGTTT 1586
           | ||| ||| | ||
Db   60773 TGTCTGGAGAGCTT 60787
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RESULT 8
US-10-995-561-13379
; Sequence 13379, Application US/10995561
; Publication No. US2005027205A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13379
; LENGTH: 14804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13379

Query Match 3.4%; Score 179.6; DB 7; Length 14804;
Best Local Similarity 80.0%; Pred. No. 1.9e-30;
Matches 224; Conservative 2; Mismatches 46; Indels 8; Gaps 1;

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Qy    1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCGTCTCAGCCTCC 1380
           | ||||||||||||||||||||||||||||||||||| ||||||||||  | |||||||
Db  13508 ATCTCAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGCCTCAGCCTCC 13567

Qy    1381 CGCGTAGCTGGGACTACAGGC-------GCACGCCCGCTAATTTTGTATTGTTAGTA 1432
           | | | ||||||| ||||||        |||| ||||  | || ||| | ||| |||
Db  13568 CAAGTAGCTGGGATTACAGGCACGCACCCAGCTAATTTTTGTATTCTTAGTA 13627

Qy    1433 GAGATGGGGTTTCACCATATTAGCCCGGATGCTGGTCTCGAACTCCTGACCTCAGTGATCCA 1492
           ||||||||||||||| |||||| || ||| || ||||||||||||||  ||||||| |||||
Db  13628 GAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAAATGATCCA 13687

Qy    1493 CCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGGGATTACACGGCGTCCGCCAAGG 1552
           |||||| |||||| | |||||  |||||  |||||||||  || ||||  | ||| |||||
Db  13688 CCCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGGGATTACAGGCGYGGCCCCGT 13747

Qy    1553 GTCAGTGTTAATAAGGAATAAACTTGAATGGTTTACTAAA 1592
           ||||||||||||| |||||  |      | ||| ||||||
Db  13748 TATTTCAKTTAGCCTCAAATACAAATATGGAGTAAGCAA 13787
```

RESULT 9

RESULT 7
US-10-995-561-13274
; Sequence 13274, Application US/10995561
; Publication No. US2005027205A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13274
; LENGTH: 415117
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(415117)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-995-561-13274

Query Match 3.5%; Score 183.4; DB 7; Length 415117;
Best Local Similarity 76.5%; Pred. No. 1.1e-30;

Query Match 3.5%; Score 184; DB 7; Length 60754;
Best Local Similarity 71.9%; Pred. No. 3.6e-31;
Matches 256; Conservative 1; Mismatches 91; Indels 8; Gaps 1;

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Qy    1283 GTGAGGGTCTGTGTCTTACACCTACCTGTATGCTTCACACCTGAGCTCACTGCAACCTCT 1342
           |||  | ||| | ||| |||||||   ||  ||||  ||||||||||||||||||||
Db    9703 GTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCGCGATCTCAGCTCACTGCAACCTCY 9644

Qy    1343 GCCTCCCAGGTTCAAGCAATTCTCCTGTATGTTAGTAGAGATGGGGTTTGGGACTACAGGCG 1402
           ||||||| |||||||| ||| |||    |||  | | | |||||||||||| ||| |||||
Db    9643 GTCTCGCTCGGGTTCAAGCGATTTTCTGCCTCAGCCTCCCAGCTAGCTGGGATTACAGGAG 9584

Qy    1403 C-------ACGCCCGGCTAATTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTG 1454
           |       || ||| |||||||||| ||||||| | | | ||| |||||||||| | |
Db    9583 CCTGTCACTATGCCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTG 9524

Qy    1455 GCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCCGGCCTCCCAAAGTG 1514
           |||| |||||| || |||||||| ||||||||||| |||||  |||| ||||||||||
Db    9523 GCCAGGCTGGTCTTGAACTCCTGACCTCAAGTGATCCACCCGCCTCCCGGCCTCCCAAAGTG 9464

Qy    1515 CTGGGATTACAGGCATGAGTCACCGCCGCCCGGCCAAGGGTCAGTGTTAATAAGGAAAA 1574
           |||||||||||||| |  |   |  |||| ||||||  |  || ||||    |   |||
Db    9463 CTGGGATTACAGGCATTAGCCACTGCCGCCCGGCCAACAATTCAAATCTTAACAAACAAAA 9404

Qy    1575 CTTGAATGGTTTACTAAACAACAGGGAAACAGACAAAAGTGTGATAAATTTCAGG 1630
           | | || |||| || ||| |  | |||   | || ||  | || ||||||||||
Db    9403 TAATAATAAATAAGAAAGAAAAGAAAAACACAAATATCAGAGCATATTACGGG 9348
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RESULT 8
US-10-995-561-13379
; Sequence 13379, Application US/10995561
; Publication No. US2005027205A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13440
; LENGTH: 60754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13440

US-10-995-561-13331/c
; Sequence 13331, Application US/10995561
; Publication No. US2005072054A1
; GENERAL INFORMATION:
;   APPLICANT: CARGILL, Michele et al.
;   TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;   TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;   TITLE OF INVENTION: DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001559
;   CURRENT APPLICATION NUMBER: US/10/995,561
;   CURRENT FILING DATE: 2004-11-24
;   NUMBER OF SEQ ID NOS: 85702
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13331
;   LENGTH: 98716
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-13331

Query Match   3.4%; Score 179.6; DB 7; Length 98716;
Best Local Similarity   80.0%; Pred. No. 4.3e-30;
Matches 224; Conservative   2; Mismatches   46; Indels   8; Gaps   1;

Qy   1321 ACCTGAGCTCACTGCAACCTGCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
           || ||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   75944 ATCTCAGCTCACTGCAACCTGCTCCCAGGTTCAAGCAATTCTCCTGCCTCAGCCTCC 75885

Qy   1381 CGCGTAGCTGGGACTACAGGC--------GCACGCCCGGCTAATTTTGTATTGTTAGTA 1432
           ||||||||||||||||||||| | |||||||||||| ||||||||||||||
Db   75884 CAAGTAGCTGGGATTACAGGCACGCACCACCGCCCAGCTAATTTTTGTATTCTTAGTA 75825

Qy   1433 GAGAGTGGGGTTTCACCATATTAGCCCGGCTGGTCTGAACCTCAGGTGATCCA 1492
           ||||| |||||||||||||| |||||||||||||| ||||||||||||||||
Db   75824 GAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAAATGATCCA 75765

Qy   1493 CCCACCTCAGCCTCCTAAAGTGCTGGGATTACAGGCGTGAGTCACCGCGCCCGGCCAAGG 1552
           |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   75764 CCCACCTCCGTCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCYGGCCCCGT 75705

Qy   1553 GTCAGTGTTTAATAAGGAATAACTTGAATGGTTTACTAAA 1592
           ||||| || || |||| |
Db   75704 TATTTCAKTTAAGCCTCAAATACAAATATGGAGTAAGCAA 75665

RESULT 10
US-11-121-086-60
; Sequence 60, Application US/11121086
; Publication No. US2005026459A1
; GENERAL INFORMATION:
;   APPLICANT: POULSEN, TIM S.
;   APPLICANT: NIELSEN, KIRSTEN V.
;   TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
;   FILE REFERENCE: 09138.6000-00000
;   CURRENT APPLICATION NUMBER: US/11/121,086
;   CURRENT FILING DATE: 2005-05-04
;   PRIOR APPLICATION NUMBER: 60/567,570
;   PRIOR FILING DATE: 2004-05-04
;   NUMBER OF SEQ ID NOS: 107
;   SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60
;   LENGTH: 191091
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-121-086-60

Query Match   3.4%; Score 179.6; DB 8; Length 191091;
Best Local Similarity   79.9%; Pred. No. 5.6e-30;
Matches 227; Conservative   0; Mismatches   49; Indels   8; Gaps   1;

Qy   1290 TCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCTCTGCCTCCC 1349
           ||||||||||||||||||| ||||||| || ||||||||||||||||||| ||||||||
Db 104701 TCTGTCCCTAGGCTGGAGTGCAGTGGCACAATCTTAGCTCACTGCACCTCCACCTCCC 104760

Qy   1350 AGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGGC------- 1401
           ||||||||||||||||||||||||||||||||| || |||| |||||||||||
Db 104761 AGGTTCCAGCAATTCTCCTGTCTCAGCCTCCCGAGTAGCTGGGACTAGCAGGCACACTA 104820

Qy   1402 GCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCGGC 1461
           |||||||||||||||||| || ||||||||||||||||||||||||||||||||||||
Db 104821 TCACGCCCATCTAATTTTTTGTATTTTTAGTGGAGACAGGGTTTCACCATATTGGTCAGGC 104880

Qy   1462 TGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCTCAAAGTGCTGGGAT 1521
           ||||| |||||||||||||||||||||||||||||||| || ||||||||||||||||
Db 104881 TGGTCTCGAACTCCTGACCTGTCAGCCTCCGCCTCCTCCGGCCTCCCAAAGTGCTGGGAT 104940

Qy   1522 TACAGGCATGAGTCACCGCGCCGGCCAAGGGTCAGTGTTTAAT 1565
           |||||||||||||||||||||||||||||||||||||||| |||
Db 104941 TACAGGCGTGAGCCACCGCCACCGAGCCCGCCGGCCCCATGTCAGTGTTATTTAAT 104984

RESULT 11
US-11-112-908-61/c
; Sequence 61, Application US/1112908
; Publication No. US2005026659A1
; GENERAL INFORMATION:
;   APPLICANT: Harris, Cole
;   APPLICANT: Davis, Lisa M.
;   TITLE OF INVENTION: Breast Cancer Biomarkers
;   FILE REFERENCE: 04-164-US
;   CURRENT APPLICATION NUMBER: US/11/112,908
;   CURRENT FILING DATE: 2005-04-22
;   PRIOR APPLICATION NUMBER: US 60/564,758
;   PRIOR FILING DATE: 2004-04-23
;   PRIOR APPLICATION NUMBER: US 60/575,978
;   PRIOR FILING DATE: 2004-06-01
;   PRIOR APPLICATION NUMBER: US 60/631,702
;   PRIOR FILING DATE: 2004-11-30
;   PRIOR APPLICATION NUMBER: US 60/633,826
;   PRIOR FILING DATE: 2004-12-07
;   NUMBER OF SEQ ID NOS: 511
;   SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
;   LENGTH: 159497
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-112-908-61

Query Match   3.4%; Score 179; DB 8; Length 159497;
Best Local Similarity   81.0%; Pred. No. 7.1e-30;
Matches 221; Conservative   0; Mismatches   50; Indels   2; Gaps   1;

Qy   1281 GGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCCACCTACACCTGAGCTCACTGCAACCT 1340
           ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db 100954 GAGTGTTGCTCTGTCGTCAACTAGGCTGGAATGCAGTGGCATGGCATCTCAGCTCACTGCAACCT 100895

Qy   1341 CTGCCTCCCAGGTTCAAGCAATTCTCCTGTCCTGTGGGACTACAGG 1400
           ||||||||||||||||| || ||||||||||||||||| |||||||
Db 100894 CTGCCTCCTGGGTTCAAGCGATTCTCAGCCTGTCTCAGCCTCCAAGTAGTTGGGATTACAGG 100835

Qy   1401 C--GCACGCCCGGCTAATTTTTGTATTTTTGTATTGTTTTCACCATATTAGCCC 1458
           | |||||||||||||||||||| |||||||||||||||||||||||||||||
Db 100834 CCACCATGCCCGGCTAATTTTTGTATTTTTTAGTAGAGATGGGGTTTCACCATGTTAGGCA 100775

Qy   1459 GGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGG 1518
           ||||||||||| ||||||| || |||||||||||||||||||| |||||||| ||||||
Db 100774 GGCTGGTCTCGAACTCCTGACCTCAAGTGATCCACTCGCCTCGCCTCGGCCTCCCAAAGTTTTGG 100715

Qy   1519 GATTACAGGCATGAGTCACCGCGCCCGGCCAAG 1551
           |||||||||||||||||||||||||||||||||
Db 100714 GATTACAGGCATGAGCCACCACTGCGGCTGCCATG 100682

RESULT 12
US-11-112-908-60/c
; Sequence 60, Application US/1112908
; Publication No. US2005026659A1

; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60
; LENGTH: 171427
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-60

Query Match   3.4%;   Score 179;   DB 8;   Length 171427;
Best Local Similarity   81.0%;   .Pred. No. 7.4e-30;
Matches   221;   Conservative   0;   Mismatches   50;   Indels   2;   Gaps   1;

Qy   1281 GGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCACACCTGAGCTCACTGCAACCT 1340
                  ||||| |||||| ||| ||||| |||||||||||||| ||||| |||| || | ||||
Db   7090 GAGTGTTGCTCTGTTGCCCAGGCTGGAATGCAGTGGCATGATCTCCGGCTCACTGCAACCT 7031

Qy   1341 CTGCCTCCCAGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGG 1400
                  |||||||||||||||||||||||||||||||||| |||||||||||||
Db   7030 CTGCCTCCTGGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCAAGTAGTTGGGATTACAGG 6971

Qy   1401 C--GCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCC 1458
                  | ||| ||| ||||||||| ||||||||||||||||||||||||||| ||
Db   6970 CCACCACGCCCGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTGTTAGGCA 6911

Qy   1459 GGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCGCCTCAGCCTCCTAAAGTGCTGG 1518
                  ||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   6910 GGCTGGTCTCGAACTCCTGACCTCAAGTGATCATCCGCCTCGGCCTCCCAAAGTTTTGG 6851

Qy   1519 GATTACAGGCATGAGTCACCCGCGCCCGGCCAAG 1551
                  |||||||||||||||||||| |||| ||||||
Db   6850 GATTACAGGCATGAGCCACCGCGCCCTGGCCATG 6818

RESULT 13
US-10-775-169-82/c
; Sequence 82, Application US/10775169
; Publication No. US20050287532A9
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dorner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 127917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-82

Query Match   3.4%;   Score 178.4;   DB 7;   Length 127917;
Best Local Similarity   77.2%;   Pred. No. 8.9e-30;
Matches   233;   Conservative   0;   Mismatches   61;   Indels   8;   Gaps   1;

Qy   1281 GGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCACACCTGAGCTCACTGCAACCT 1340
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   99645 GAGTCTTGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCATGATCTCCGGCTCACTGCAAACT 99586

Qy   1341 CTGCCTCCCAGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGG 1400
                  ||||||||||||||||||||||||||||||||
Db   99585 CCACCTCCCAAGTTCAAGCGATTCTCCTGTCTCAGCCTCCCGAGTAGCTGGGATTACAGG 99526

Qy   1401 CG-------CACGCCCACCACCCAGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATAT 1452
                  || |||||||| ||||||||||||||||||||||||||||||||||
Db   99525 TGCCCACCACCACCCAGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATAT 99466

Qy   1453 TAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCACCTCAGCCTCCTAAAG 1512
                  |||||||||||||||||||| |||||| |||||| |||||||||||||
Db   99465 TGGCCAGACTGGTCTCGAACTCCTGACCTCGGGTGATCCACCCGCCTCAGCCTCCCCAGG 99406

Qy   1513 TGCTGGGATTACAGGCGTCAGTGTTTAATAAGGAAT 1572
                  |||||||||||||| | |||||| |||||||||
Db   99405 TGCTGGGATTATAGGCGTGAGCCACCGCGCCTTTTAAAGGAAGG 99346

Qy   1573 AA 1574
                  ||
Db   99345 AA 99344

RESULT 14
US-11-112-908-57
; Sequence 57, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57
; LENGTH: 161994
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-57

Query Match   3.4%;   Score 177.8;   DB 8;   Length 161994;
Best Local Similarity   86.0%;   Pred. No. 1.3e-29;
Matches   197;   Conservative   0;   Mismatches   32;   Indels   0;   Gaps   0;

Qy   1325 GAGTCCACTGCAACCTCTGCCTCCCAGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCG 1384
                  ||||| |||| | |||||||||||| ||||||||||| ||||||||||||||||||||||
Db   131831 GAGTGCAATGCGAGCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAG 131890

Qy   1385 TAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTT 1444
                  ||||||||||||||||| | ||||||||||||||| ||||| ||||||||||||||||
Db   131891 TAGCTGGGATTACAGGCGCCCAGCCCAGCTAATTTTTTATATTTTTAGTAGAGATGGGGTTT 131950

Qy   1445 CACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCC 1504
                  |||||| ||||||| ||||||||| |||||||||| |||| ||||| | ||||||||||
Db   131951 CACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACTTCAGGTGATCTGCCCGCCTCGGCC 132010

Qy   1505 TCCTAAAGTGCTGGGATTACAGGCGTGAGTCACCGCGCCCGGCCAAGGG 1553
                  |||| |||||||||||||||||||||||| ||||||||||| ||||||
Db   132011 TCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCGCCCGCCAAGGG 132059

RESULT 15
US-11-112-908-59
; Sequence 59, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
;   APPLICANT: Harris, Cole
;   APPLICANT: Davis, Lisa M.
;   TITLE OF INVENTION: Breast Cancer Biomarkers
;   FILE REFERENCE: 04-164-US
;   CURRENT APPLICATION NUMBER: US/11/112,908
;   CURRENT FILING DATE: 2005-04-22
;   PRIOR APPLICATION NUMBER: US 60/564,758
;   PRIOR FILING DATE: 2004-04-23
;   PRIOR APPLICATION NUMBER: US 60/575,978
;   PRIOR FILING DATE: 2004-06-01
;   PRIOR APPLICATION NUMBER: US 60/631,702
;   PRIOR FILING DATE: 2004-11-30
;   PRIOR APPLICATION NUMBER: US 60/633,826
;   PRIOR FILING DATE: 2004-12-07
;   NUMBER OF SEQ ID NOS: 511
;   SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59
;   LENGTH: 168656
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-112-908-59

Query Match   3.4%;   Score 177.8; DB 8;   Length 168656;
Best Local Similarity 86.0%; Pred. No. 1.4e-29;
Matches 197; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 1325 GAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCGTGTCTCAGCCTCCCGCG 1384
          || ||||||||||||||||||| ||||||||||||| ||||||| ||||| ||||||||
Db 1285 GAGTGCAATGCGAGCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAG 1344

Qy 1385 TAGCTGGGACTACAGGCGCACGCCCGGCCTAATTTTGTATTGTTAGTAGAGATGGGGTTT 1444
          || ||||||| |||||| ||| |||| |||| |||||||||| ||||||||||||||||
Db 1345 TAGCTGGGATTACAGGGGCAGGCCCAGCTAATTTTATATTTTTAGTAGAGATGGGGTTT 1404

Qy 1445 CACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCACCTCAGCC 1504
          |||| || ||| |||||||||||||||||||| |||||| || ||| || ||||||
Db 1405 CACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCTCAGGCAGTCTCGCCCGCCTGGGCC 1464

Qy 1505 TCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGG 1553
          |||||||||||||||||||||||| |||||| |||||||| ||||||||
Db 1465 TCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCGCCCGGGCCAAGGG 1513

Search completed: January 26, 2006, 10:16:38
Job time : 525 secs

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                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:       January 26, 2006, 02:50:21 ; Search time 17273 Seconds
                            (without alignments)
                            16872.686 Million cell updates/sec

Title:          US-09-227-881-34
Perfect score:  5271
Sequence:       1 atctttgttcagttacctc.........tcgggcatgagggcagcaagg 5271

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters:        158295336

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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         9:  /cgn2_6/ptodata/1/pna/US079_COMB.seq:*
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        11:  /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
        12:  /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
        13:  /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
        14:  /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
        15:  /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
        16:  /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5271	100.0	5271	22	US-09-227-881-34	Sequence 34, Appl
2	5271	100.0	5271	43	US-10-244-633-34	Sequence 34, Appl
3	5271	100.0	6169	19	US-08-938-669-3	Sequence 3, Appli
4	5271	100.0	6169	22	US-09-227-881-3	Sequence 3, Appli
5	5271	100.0	6169	43	US-10-244-633-3	Sequence 3, Appli
6	5246.4	99.5	5300	19	US-08-938-669-1	Sequence 1, Appli
7	5246.4	99.5	5300	22	US-09-227-881-1	Sequence 1, Appli
8	5246.4	99.5	5300	38	US-09-985-637A-1	Sequence 1, Appli
9	5246.4	99.5	5300	43	US-10-244-633-1	Sequence 1, Appli
10	5246.4	99.5	5300	61	US-10-741-339-1	Sequence 1, Appli
11	5232.4	99.3	37252	40	US-10-087-192-1228	Sequence 1228, Ap
12	5224.4	99.1	5304	19	US-08-938-669-2	Sequence 2, Appli
13	5224.4	99.1	5304	22	US-09-227-881-2	Sequence 2, Appli
14	5224.4	99.1	5304	43	US-10-244-633-2	Sequence 2, Appli
15	4925.4	93.4	7369	75	US-60-172-360-23886	Sequence 23886, A
16	4017.4	76.2	6000	52	US-10-509-595-1	Sequence 1, Appli
17	1804.4	34.2	2800	23	US-09-366-952-1	Sequence 1, Appli
18	1804.4	34.2	2800	43	US-10-278-698-294	Sequence 294, App
19	1804.4	34.2	2800	43	US-10-278-698-808	Sequence 808, App
20	1804.4	34.2	2800	62	US-10-803-557-10	Sequence 10, Appl
21	1804.4	34.2	2800	64	US-10-956-243-1	Sequence 1, Appli
22	1691.6	32.1	2666	17	US-08-791-154-3	Sequence 3, Appli
23	1690	32.1	2397	17	US-08-791-154-1	Sequence 1, Appli

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24   1669.6   31.7   1950   17   US-08-791-154-2           Sequence 2, Appli
25    631.6   12.0    632   36   US-09-925-065A-905501     Sequence 905501,
26    629.6   11.9    630   36   US-09-925-065A-917000     Sequence 917000,
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29    548     10.4    573   46   US-10-301-480A-794512     Sequence 794512,
30    548     10.4    573   47   US-10-301-480B-794512     Sequence 794512,
31    548     10.4    573   48   US-10-301-480C-794512     Sequence 794512,
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34    432.6    8.2   2313   82   US-60-680-544-5473        Sequence 5473, Ap
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42    394.4    7.5   1086   43   US-10-240-425-1586        Sequence 1586, Ap
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44    394.4    7.5   1086   61   US-10-756-149-932         Sequence 932, App
45    393      7.5    545   36   US-09-925-065A-346050     Sequence 346050,
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ALIGNMENTS

RESULT 1
US-09-227-881-34
; Sequence 34, Application US/09227881
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/227,881
; CURRENT FILING DATE: 1999-01-11
; EARLIER APPLICATION NUMBER: US 08/938,669
; EARLIER FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 34
; LENGTH: 5271
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-227-881-34

  Query Match   100.0%;   Score 5271;   DB 22;   Length 5271;
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  Matches 5271;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   61 TCCTATAAACTGTATAGCCTCAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAGTG   120
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Qy   121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA   180
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Qy   181 CAGATGTTGCTTCCTGACAGAAGAGCTATTCTTCAGGAAACATCACATCCCAATGTGAAATC   240
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Qy   241 CATCAAACAGGAGCTAAGAAACAGAGAATGGGCACTTGCCCAAGGAAAAATGCCAG   300
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Qy   661 AGTGATTAGGCAGTTGACCATGTTGCCGCAACACCTCCCGTCTATACCAGGAACACAAAAA   720
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Qy   721 ATTGACTGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAATGAGAAACAAAAAACAAAA   780
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Qy   781 GACATGGTTAAAAGGCAACCAACCAGCACTTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA   840
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Qy   901 TTGAAAGATCATGAATTTTAACCATTTAAGTATAAAACAAATATGCGATAATGCATAATCAG   960
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Qy   961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATCACAAGGATAACGTGTCCCAGCTCC   1020
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Qy   1081 TGTCATAGCCCTCACACACAGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA   1140
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Qy   1201 TGTGCAGCCCATCCCGCTCCACAGAGAGTCTCCCCACTCTAGACTTCTGCATCACGAGTGT   1260
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Qy   1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTCTTCACCTACCTAC   1320
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Qy   1321 ACCTGAGCTCACTGCAACCTCTGCCTCCGCAATTCTCCGTGTCTCAGCCTCC   1380
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Qy   1381 CGCCGTAGCTGGGACTACAGGCGCGCACCCGCCGCTAATTTTGTATTGTTAGTAGAGATGGG   1440
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Db   1381  CGCGTAGCTGGGACTACAGGCGCCCGGCCTAATTTTGTATTGGTTAGTAGAGATGGG  1440
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Db   1441  GTTTCACCATATTAGCCCGGGCTGGTCTTGAACTCCTGACCTCAGGTGATCACCCACCTC  1500
Qy   1501  AGCCTCCTAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCAAGGGTCAGTGT  1560
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Qy   1561  TTAATAGGAATAACTTGAATGGTTTACTAAACCAACAGACAAAGCTGTGA  1620
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Qy   1621  TAATTTCAGGGATTCTTGGGATGGGAATGGTGCCATGAGCTGCCTAGTCCCTAGAGAC  1680
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Db   1681  CACTGGTCCTCATCACTTTCTTCCCTCATCCCTCATTTTCAGGCTAAGTTACCATTTTATT  1740
Qy   1741  CACCATGTCTTTGTGGTAAGCCTTCCACATGCGTTACTGAAATAAGAGTATACATAAACTAG  1800
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Qy   1801  TTCCATTTGGGCCATCTGTGTGTGTATAGGGGAGGAGGGCATACCCCCAGAGACTCCT  1860
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Db   1801  TTCCATTTGGGCCATCTGTGTGTGTATAGGGGAGGAGGGCATACCCCCAGAGACTCCT  1860
Qy   1861  TGAAGCCCCCGGCAGAGTTTCCTCCAGTGGGGGAGCCCTGCAAGCAGTCACTGC  1920
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Db   1861  TGAAGCCCCCGGCAGAGTTTCCTCCAGTGGGGGAGCCCTGCAAGCAGTCACTGC  1920
Qy   1921  TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG  1980
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Db   1921  TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG  1980
Qy   1981  GACCTGTTGCTTTCTATTTCTGTGTGTGACTCGTTCATTCCAGGCCATTCATTGACAATT  2040
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Db   1981  GACCTGTTGCTTTCTATTTCTGTGTGTGACTCGTTCATTCCAGGCCATTCATTGACAATT  2040
Qy   2041  TATTGAGTACTTATATCTGCCAGACACCAGACAAAATGTGAGCAAGCAGTCACTGC  2100
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Qy   2101  CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAGAAATTAATAGCCA  2160
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Qy   2161  GCCAACTTAAACCCAGTGCTGAAAGAAGAAATAAACACCATCTTGAAGAATTGTCGGC  2220
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Qy   2221  AGCATCCCTTAACAAGGCCACCTCCCAGCCTCCTCCCTCGCGCCCCTGCCCAGCGGCTGGCCT  2280
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Qy   2281  CCCCAAGCCCGGACCCTTCCCGAATCGTCCTGTCATCTGAGCTGAGACTCTGCCCGGCT  2340
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Qy   2341  CCAGAAAGGAAATGGAGAGGGAAATCGAGGGGAACTAGTCTTAACGGAGGGGGACAGTGTTTC  2400
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Qy   2521  TGGGGACGCTGGGGCTGAGCGGTGCTGAAAGGCAGGAGGTGCAAGGCTGAA  2580
                  |||||||||||||||||||||||||||||||||||||||||||||
Db   2521  TGGGGACGCTGGGGCTGAGCGGTGCTGAAAGGCAGGAGGTGCAAGGCTGAA  2580
Qy   2581  GCTGCCCAGATGTTCAGTGTTCTTCACGGGGCTGGGAGTTTCCGTTGCTTCCTGTGAGC  2640
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  GCTGCCCAGATGTTCAGTGTTGTTCACGGGGTGGGAGTTTCCGTTGCTTCCTGTGAGC  2640
Qy   2641  CTTTTATCTTTTCTCTGCTTGGAGGAGAAGAGTCTATTTCATGAAGGGATGGATGCAGTTTC  2700
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  CTTTTATCTTTTCTCTGCTTGGAGGAGAAGAGTCTATTTCATGAAGGGATGGATGCAGTTTC  2700
Qy   2701  ATAAAGTCAGCTGTTAAAATTCCAGGGTGCATGGGTTTCCTTCACGAAGGCCTTTAT  2760
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  ATAAAGTCAGCTGTTAAAATTCCAGGGTGCATGGGTTTCCTTCACGAAGGCCTTTAT  2760
Qy   2761  TTAATGGAATATAGGAAGCGAGCTCATTCCTCAGGCCGTTAATTCACGGGAAGTGAC  2820
                  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  TTAATGGAATATAGGAAGCGAGCTCATTCCTCAGGCCGTTAATTCACGGAAGAAGTGAC  2820
Qy   2821  TGGAGTCTTTCTTCTCATGTCTTCGGGCAACTACTCAGCCCTGGTGGACTTGGCTTA  2880
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  TGGAGTCTTTCTTCTCATGTCTTCGGGCAACTACTCAGCCCTGGTGGACTTGGCTTA  2880
Qy   2881  TGCAAGACGGTCGAAAACCTTGAAATCAGGAGACTCGGTTTCTTCCTCGGGCCATAGTCTTCTCTGCT  2940
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  TGCAAGACGGTCGAAAACCTTGAAATCAGGAGACTCGGTTTCTTCCTCGGGCCATAGTCTTCTCTGCT  2940
Qy   2941  GGTTGGCTGTGCGGCAGAGCCAGGCAGCAGCAGGAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC  3000
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  GGTTGGCTGTGCGGCAGAGCCAGGCAGCAGCAGGAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC  3000
Qy   3001  ATAAAGACCCTTGCAGCTCTCGTTCTGTTCTGTGTTCTCTGTGAACACTTCCCTGATTCTCTGTGAGGGG  3060
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  ATAAAGACCCTTGCAGCTCTCGTTCTGTTCTGTGTTCTCTGTGAACACTTCCCTGATTCTCTGTGAGGGG  3060
Qy   3061  GGATGTGTTGAGAGGGAGGAGGGAGCCAGCAGCTGGAGCTGGAGTGGAGGG  3120
                  |||||||||||||||||||||||||||||||||||||||||||||||
Db   3061  GGATGTGTTGAGAGGGAGGAGGGAGCCAGCAGCTGGAGCTGGAGTGGAGGG  3120
Qy   3121  GGACAGGAAGCCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC  3180
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121  GGACAGGAAGCCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC  3180
Qy   3181  CAGGACCGAGAGCCACACAATGCTCAGGAAAGCTCAATGAACCCAACAGCAGCCACATTTTCCT  3240
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181  CAGGACCGAGAGCCACACAATGCTCAGGAAAGCTCAATGAACCCAACAGCAGCCACATTTTCCT  3240
Qy   3241  TCCCTAAGCATAGACAATGGCATTGCCAATAACCAAAAGATGCAGAGACTAACTGGT  3300
                  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241  TCCCTAAGCATAGACAATGGCATTGCCAATAACCAAAAAGATGCAGAGACTAACTGGT  3300
Qy   3301  GGTAGCTTTTGCTTGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG  3360
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301  GGTAGCTTTTGCTTGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG  3360
Qy   3361  TTAAACTTTTCACCCTGCAGCTCCAGGCTCTGAGCTGACCAGTGTATGAGCAGAAAG  3420
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361  TTAAACTTTTCACCCTGCAGCTCCAGGCTCTGAGCTGACCAGTGTATGAGCAGAAAG  3420
Qy   3421  AGTGACCTGCAGGGGACGCAGGGGAGAGAAAGAGAGGGATGGATGTGTGAGCACGACACG  3480
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421  AGTGACCTGCAGGGGACGCAGGGGAGAGAAAGAGAGGGATGGATGTGTGAGCACGAAGACG  3480
Qy   3481  ACAGATTCATTCAAGGGACCAGTGCAGTTGACCACCACAGGGATTATTAGTCCACGTGATCGTTGG  3540
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481  ACAGATTCATTCAAGGGACCAGTGCAGTTGACCACCACAGGGATTATTAGTCCACGTGATCGTTGG  3540
Qy   3541  GTTCTAGGAGCAGGGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGTCGGGAGA  3600
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541  GTTCTAGGAGCAGGGGCTATATTGTGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA  3600
```

RESULT 2
US-10-244-633-34
; Sequence 34, Application US/10244633
; GENERAL INFORMATION:
;   APPLICANT: Nguyen, Thai D.
;   APPLICANT: Polansky, Jon R.
;   APPLICANT: Chen, Pu
;   APPLICANT: Chen, Hua
;   TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
;   TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
;   TITLE OF INVENTION: Disorders
;   FILE REFERENCE: 07425.0057.US01
;   CURRENT APPLICATION NUMBER: US/10/244,633
;   CURRENT FILING DATE: 2002-09-17
;   PRIOR APPLICATION NUMBER: US/09/306,828
;   PRIOR FILING DATE: 1999-05-07
;   PRIOR APPLICATION NUMBER: US 09/227,881
;   PRIOR FILING DATE: 1999-01-11
;   NUMBER OF SEQ ID NOS: 38
;   SOFTWARE: Microsoft Word 97
; SEQ ID NO 34
;   LENGTH: 5271
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-244-633-34

Query Match   100.0%; Score 5271; DB 43; Length 5271;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 5271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATCTTTGTTCAGTTACCTCAGGCTATTATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATCTTTGTTCAGTTACCTCAGGCTATTATGAGATAACCAATGTGAAAG 60

Right column block (positions 1141–2280):

```
Qy  1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCATTCAGCCTCC  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCATTCAGCCTCC  1200

Qy  1201  TGTGCAGCCCATCCCGCTCCACAGAGAAGTCTCCCCACTCTCGATCACGATGT  1260
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  TGTGCAGCCCATCCCGCTCCACAGAGAAGTCTCCCCACTTCTCGATCACGATGT  1260

Qy  1261  TACAGCCAGAAGTCTCCGTGAGGGTGAGGGTCGTGTCTTACACCTACCTGTATGCTCTAC  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  TACAGCCAGAAGTCTCCGTGAGGGTGAGGGTCGTGTCTTACACCTACCTGTATGCTCTAC  1320

Qy  1321  ACCTGAGCTCACTGCAACCTGCTCCGCTCCCAGGTCAAGCAATTCTCCTGTCTCAGCCTCC  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  ACCTGAGCTCACTGCAACCTGCTCCGCTCCCAGGTCAAGCAATTCTCCTGTCTCAGCCTCC  1380

Qy  1381  CGCGTAGCTGGGACTACAGGCGCACGCCCGCTAATTTTGTATTGTTAGTAGAGATGGG  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CGCGTAGCTGGGACTACAGGCGCACGCCCGCTAATTTTGTATTGTTAGTAGAGATGGG  1440

Qy  1441  GTTTCACCATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGTGATCCACCCACCTC  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  GTTTCACCATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGTGATCCACCCACCTC  1500

Qy  1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT  1560

Qy  1561  TTAATAAGGAATAACTTGAATGTTACTAAACCAACAGGGAAAACAGACAAAAGCTGTGA  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  TTAATAAGGAATAACTTGAATGTTACTAAACCAACAGGGAAAACAGACAAAAGCTGTGA  1620

Qy  1621  TAATTTCAGGGATTCTTCGGGATGGGAATGGTGCCATGGGGGGAGGGGCATACCCCAGACTCCT  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  TAATTTCAGGGATTCTTCGGGATGGGAATGGTGCCATGGGGGGAGGGGCATACCCCCAGAC  1680

Qy  1681  CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGGCTAAGTTACCATTTTATT  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGGCTAAGTTACCATTTTATT  1740

Qy  1741  CACCATGCTTTTGTGTGGTAAGCCTCCACATCGTTACTGACTGAAATAGAGTATACATAAACTAG  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  CACCATGCTTTTGTGTGGTAAGCCTCCACATCGTTACTGACTGAAATAGAGTATACATAAACTAG  1800

Qy  1801  TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGGGCATACCCCCAGAGACTCCT  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGGGCATACCCCCAGAGACTCCT  1860

Qy  1861  TGAAGCCCCCGGCAGAGAGTTTCCTCTCGAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  TGAAGCCCCCGGCAGAGAGTTTCCTCTCGAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC  1920

Qy  1921  TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTGTGTTTGTTATCACTCTCTAGG  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTGTGTTTGTTATCACTCTCTAGG  1980

Qy  1981  GACCTGTTGCTTCTATTTCTATTTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  GACCTGTTGCTTCTATTTCTATTTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT  2040

Qy  2041  TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGAGTCACTGC  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGAGTCACTGC  2100

Qy  2101  CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGAGACGTGAGCGAGAAGAAATTAATAGCCA  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGAGACGTGAGCGAGAAGAAATTAATAGCCA  2160

Qy  2161  GCCAACTTAAACCCAGTGCTGCTAAAGAAATAAACCATCTTGAAGAATTGTGCGC  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GCCAACTTAAACCCAGTGCTGCTAAAGAAATAAACACCATCTTGAAGAATTGTGCGC  2220

Qy  2221  AGCATCCCTTAACAAGGCCACCTCCCTTAACAAGGCCCCCCCTTGCTCGTCGTCCCGGAGG  2280
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Left column block (positions 61–1140):

```
Qy    61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA   120

Qy   121  GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTTTATTTTAGTGA   180
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTTTATTTTAGTGA   180

Qy   181  CAGATGTTGCTTCCTGACAGAAGAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC   240
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  CAGATGTTGCTTCCTGACAGAAGAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC   240

Qy   241  CATCAAACAGGAGCTAAGAAAACAGGAATGGATGGCACTTGCCCAAGGAAAAATGCCAG   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  CATCAAACAGGAGCTAAGAAAACAGGAATGGATGGCACTTGCCCAAGGAAAAATGCCAG   300

Qy   301  GAGAGCAATAATGATGAAAAATAAACTTTCCCTTTGTTTTAATTTCAGGAAAAATG   360
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  GAGAGCAATAATGATGAAAAATAAACTTTCCCTTTGTTTTAATTTCAGGAAAAATG   360

Qy   361  ATGAGGACCAAAATCAATGAATAACAGCTCAGAAAAAGATGTTTCCAAATTGG   420
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  ATGAGGACCAAAATCAATGAATAACAGCTCAGAAAAAGATGTTTCCAAATTGG   420

Qy   421  TAATTAAGTATTTGTTCCTTGGGAAGACCCTCCATGTGAGCTTGATGGGAAAAATGGGAA   480
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  TAATTAAGTATTTGTTCCTTGGGAAGACCCTCCATGTGAGCTTGATGGGAAAAATGGGAA   480

Qy   481  AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT   540
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT   540

Qy   541  GGCATCACTCTGGGGAGGCAAGTTCGCAGAAGTTCATGTTAGCAAAGGACATAACAATAAC   600
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GGCATCACTCTGGGGAGGCAAGTTCGCAGAAGTTCATGTTAGCAAAGGACATAACAATAAC   600

Qy   601  AGCAAAATCAAAATCCCGCAAATGCAGGAGGAAATGGGACTGGGAAAGCTTTCATAAAC   660
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  AGCAAAATCAAAATCCCGCAAATGCAGGAGGAAATGGGACTGGGAAAGCTTTCATAAAC   660

Qy   661  AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATAACCAGGGAACACAAAA   720
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATAACCAGGGAACACAAAA   720

Qy   721  ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAGAGCAAAAACAAAA   780
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAGAGCAAAAACAAAA   780

Qy   781  GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCCAGTGCCCTCAGCA   840
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCCAGTGCCCCTCAGCA   840

Qy   841  GGGACCCTGAGGCATTTGCCTTTGGAAGGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC   900
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  GGGACCCTGAGGCATTTGCCTTTGGAAGGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC   900

Qy   901  TTGAAAGATCATGATGAATTTTAACCATTTAAGTAGTATAAAACAAATATGCGATGCATAATCAG   960
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  TTGAAAGATCATGATGAATTTTAACCATTTAAGTAGTATAAAACAAATATGCGATGCATAATCAG   960

Qy   961  TTTAGACATGGTCCCAATTTATAAAGTCAGGCATACAAGGATAACGTGTCCCGGTCC  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  TTTAGACATGGTCCCAATTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020

Qy  1021  GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTTAAACTTTTCAGAATGATC  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTTAAACTTTTCAGAATGATC  1080

Qy  1081  TGTCATAGCCCTGACGTGTCTGACTTACAACCACCATCTACAACCCAA  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  TGTCATAGCCCTCACACAGCCCGATGTGTCTGACTTACAACCTACAACCACCCAA  1140
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Right column:

```
Db  3301  GGTAGCTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGAAAAATGCCAGAGATTG  3360
Qy  3361  TTAAACTTTCACCCTGACCAGCACCCCACGAGCTCAGCAGTGACTGCTGACAGCACGG  3420
Db  3361  TTAAACTTTCACCCTGACCAGCACCCCACGAGCTCAGCAGTGACTGCTGACAGCACGG  3420
Qy  3421  AGTGACCTGCAGCGCGCAGGGGAGCGGGAGGAGGAGAAAAGAGACGGATAGTAGTGATGAGCAAGAAAG  3480
Db  3421  AGTGACCTGCAGCGCGCAGGGGAGCGGGAGGAGGAGAAAAGAGACGGATAGTAGTGATGAGCAAGAAAG  3480
Qy  3481  ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGATTATAGTCACGTGATCCTGG  3540
Db  3481  ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGATTATAGTCACGTGATCCTGG  3540
Qy  3541  GTTCTAGGAGGCAGGGCTATATTGTGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA  3600
Db  3541  GTTCTAGGAGGCAGGGCTATATTGTGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA  3600
Qy  3601  CCTGATTTCTAATACTATATTTTCCTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG  3660
Db  3601  CCTGATTTCTAATACTATATTTTCCTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG  3660
Qy  3661  GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAGAACTCTTTTTCTGT  3720
Db  3661  GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAGAACTCTTTTTCTGT  3720
Qy  3721  GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAGAGAAAACATTCCTAAGAG  3780
Db  3721  GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAGAGAAAACATTCCTAAGAG  3780
Qy  3781  TAAAGCCAAAACAGATTCAAGCCTAGGTCTTGCTTGCGTGACTATATGATTGGTTTTTGAAAAAT  3840
Db  3781  TAAAGCCAAAACAGATTCAAGCCTAGGTCTTGCTTGCGTGACTATATGATTGGTTTTTGAAAAAT  3840
Qy  3841  CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTAGACAAACTGTGTTTCTTCCACATCGTGTTGGTATTAACACACTGTTGTT  3900
Db  3841  CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTAGACAAACTGTGTTTCTTCCACATCGTGTTGGTATTAACACACTGTTGTT  3900
Qy  3901  TAAACAAACACCCAGTGTAAATGTCTCAGGCTTAAAGTTCAGGCTTAAAGTGTAAAATGTCTAAAGTTGTAAAAGTGTAAAAAT  3960
Db  3901  TAAACAAACACCCAGTGTAAATGTCTCAGGCTTAAAGTTCAGGCTTAAAGTGTAAAATGTCTAAAGTTGTAAAAGTGTAAAAAT  3960
Qy  3961  AGAATAGAATCTTTAGAGCAAACTGTGTTTCTTCCACATCGTGTTGGTATTAACACTGTTGTTGGTATTAACATAAAGT  4020
Db  3961  AGAATAGAATCTTTAGAGCAAACTGTGTTTCTTCCACATCGTGTTGGTATTAACACTGTTGTTGGTATTAACATAAAGT  4020
Qy  4021  AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTAAAGTTACTTCTGACAGTTTTGGTATAT  4080
Db  4021  AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTAAAGTTACTTCTGACAGTTTTGGTATAT  4080
Qy  4081  TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTTAATGTAAAGCAG  4140
Db  4081  TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTTAATGTAAAGCAG  4140
Qy  4141  TTATTGGCTATTGCCATTTGCCATTTGCTTTTGTTTTTTGTTTATTGGGTTTATTAATGTAAAGCAG  4200
Db  4141  TTATTGGCTATTGCCATTTGCCATTTGCTTTTGTTTTTTGTTTATTGGGTTTATTAATGTAAAGCAG  4200
Qy  4201  GGATTATTAACCTACAGTCCAGAAAGCCTGAATTGAATGAGGAAAAAAATTACATTTT  4260
Db  4201  GGATTATTAACCTACAGTCCAGAAAGCCTGAATTGAATGAGGAAAAAATTACATTTT  4260
Qy  4261  TGTTTTTACCACCTTCTAACTAAATTAACATTTATTCCATTGCGAATAGAGCCATAAA  4320
Db  4261  TGTTTTTACCACCTTCTAACTAAATTAACATTTATTCCATTGCGAATAGAGCCATAAA  4320
Qy  4321  CTCAAAGTGGTAATAACAGTACCTGTGCAGATACGTTGTTCAGATACGTTAAGTGAAATATTTATACTCAAAACTA  4380
Db  4321  CTCAAAGTGGTAATAACAGTACCTGTGCAGATACGTTGTTCAGATACGTTAAGTGAAATATTTATACTCAAAACTA  4380
Qy  4381  TTATACTATATTACAGTTGTTGCAGATACGTTGTTCAGATACGTTGTTCAGATACGTTGTTCAGATACGTTAAGTGAAATATTTATACTCAAAACTA  4440
Db  4381  TTATACTATATTACAGTTGTTGCAGATACGTTGTTCAGATACGTTAAGTGAAATATTTATACTCAAAACTA  4440
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Left column:

```
Db  2221  AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCTCCGTGCTCCATCGTCGTCCCCGAGG  2280
Qy  2281  CCCCCAAGCCCGAGTCTTCCAAGCCTCCTTGGTGCATCGTGCCTGGTCAGCTGCGCCT  2340
Db  2281  CCCCCAAGCCCGAGTCTTCCAAGCCTCCTTGGTGCATCGTGCCTGGTCAGCTGCGCCT  2340
Qy  2341  GCCTCGCTTCCCGTGAATCGTCCGTGAATCGTGCCTGGTGAGCTGAGCTGGAGACTCTTGGCTCCAGGCT  2400
Db  2341  GCCTCGCTTCCCGTGAATCGTCCGTGAATCGTGCCTGGTGAGCTGAGCTGGAGACTCTTGGCTCCAGGCT  2400
Qy  2401  CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGAGGAAATCTGGAGGGACAGTGTTTC  2460
Db  2401  CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGAGGAAATCTGGAGGGACAGTGTTTC  2460
Qy  2461  CTCAGAGGGGAAAGGGGCCTCACGTCCAGGAGGTGCTGCAGGTGGGGCTGCAGGGAG  2520
Db  2461  CTCAGAGGGGAAAGGGGCCTCACGTCCAGGAGGTGCTGCAGGTGGGGCTGCAGGGAG  2520
Qy  2521  TGGGGACGCTGGGGCTGAGCGGCTGGGGGCTGAAAAGGCAGGAAAGGGCAAGGCTGAA  2580
Db  2521  TGGGGACGCTGGGGCTGAGCGGCTGGGGGCTGAAAAGGCAGGAAAGGGCAAGGCTGAA  2580
Qy  2581  GCTGCCCAGATGTTCAGTTGTTGTTCACGGGCTGGGAGTTTTCCGTTGCTTCCGTGTCAGC  2640
Db  2581  GCTGCCCAGATGTTCAGTTGTTGTTCACGGGCTGGGAGTTTTCCGTTGCTTCCGTGTCAGC  2640
Qy  2641  CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAGTCTATTTCATGAAGGGATGCAGTTTC  2700
Db  2641  CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAGTCTATTTCATGAAGGGATGCAGTTTC  2700
Qy  2701  ATAAAGTCAGCTGTTAAAATTCCAGGGTGTCATGGGTTTTCCTTCACGCAGAAGGCCTTTAT  2760
Db  2701  ATAAAGTCAGCTGTTAAAATTCCAGGGTGTCATGGGTTTTCCTTCACGCAGAAGGCCCTTTAT  2760
Qy  2761  TTAATGGGAATATAGGAAGCGAGCTGCAAGTCAGGAGACTCGGTTTCTTTTCTTTGGTTTTTCTTTCTTGGTTCTGCATT  2820
Db  2761  TTAATGGGAATATAGGAAGCGAGCTGCAAGTCAGGAGACTCGGTTTCTTTTCTTTGGTTTTTCTTTCTTGGTTCTGCATT  2820
Qy  2821  TGGAGTCTTTTCTTTCATGTCTTCTCGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA  2880
Db  2821  TGGAGTCTTTTCTTTCATGTCTTCTCGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA  2880
Qy  2881  TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTCTTTCTTTGGTTTTCTTTCTTTCTGCATT  2940
Db  2881  TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTCTTTCTTTGGTTTTCTTTCTTTCTGCATT  2940
Qy  2941  GGTTGGCTGTGCCAAGTCGGGTGGGCAAGTGGTGGTCTCCATCATCTGTGTTCTCTGTGAACACTTCCCTGTGAACTTTCCT  3000
Db  2941  GGTTGGCTGTGCCAAGTCGGGTGGGCAAGTGGTGGTCTCCATCATCTGTGTTCTCTGTGAACACTTCCCTGTGAACTTTCCT  3000
Qy  3001  ATAAAGACCCTTGCAGCTCTCGTCGTCTCGTGTTCTCCCGTGAACACTTCCCTGTGAACTTCCCT  3060
Db  3001  ATAAAGACCCTTGCAGCTCTCGTCGTCTCGTGTTCTCCCGTGAACACTTCCCTGTGAACTTCCCT  3060
Qy  3061  GGATGGTTGAGAGGGAAGGGCAGGAGAGGGACAGAGGGCTGAGCGCTGGAGAGGTGGAGGGG  3120
Db  3061  GGATGGTTGAGAGGGAAGGGCAGGAGAGGGACAGAGGGCTGAGCGCTGGAGAGGTGGAGGGG  3120
Qy  3121  GGACAGGAAGGCAGGCAGGGCAGGGCAGAGCTGGGTGGCTGCTCCATCAGTCGGTGTGCTCACTGTCGATCACGTCGATCAGACTC  3180
Db  3121  GGACAGGAAGGCAGGCAGGGCAGGGCAGAGCTGGGTGGCTGCTCCATCAGTCGGTGTGCTCACTGTCGATCACGTCGATCAGACTC  3180
Qy  3181  CAGGACCGAGAGCCCACAATGCTTCGCAATGGCATTTGCCAATAACCCAACAGCCCACATTTTCCT  3240
Db  3181  CAGGACCGAGAGCCCACAATGCTTCGCAATGGCATTTGCCAATAACCCAACAGCCCACATTTTCCT  3240
Qy  3241  TCCCTAAGCATAGACAATGGCCATTTGCCATTTGCCAATAACCCAACAGCCCACATTTTCCT  3300
Db  3241  TCCCTAAGCATAGACAATGGCCATTTGCCATTTGCCAATAACCCAACAGCCCACATTTTCCT  3300
Qy  3301  GGTAGCTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGAAAAATGCCAGAGATTG  3360
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;  COUNTRY: USA
;  ZIP: 20004-2402
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE: Diskette
;    COMPUTER: IBM Compatible
;    OPERATING SYSTEM: DOS
;    SOFTWARE: FastSEQ for Windows Version 2.0
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/938,669
;    FILING DATE:
;    CLASSIFICATION: 435
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: 08/791,154
;    FILING DATE: 28-JAN-1997
;  ATTORNEY/AGENT INFORMATION:
;    NAME: Sira, Serge
;    REGISTRATION NUMBER: 39,445
;    REFERENCE/DOCKET NUMBER: 07425-0034
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE: 202 383-6857
;    TELEFAX: 202 383-6610
;    TELEX:
;  INFORMATION FOR SEQ ID NO: 3:
;  SEQUENCE CHARACTERISTICS:
;    LENGTH: 6169 base pairs
;    TYPE: nucleic acid
;    STRANDEDNESS: single
;    TOPOLOGY: linear
US-08-938-669-3

Query Match          100.0%;   Score 5271;   DB 19;   Length 6169;
Best Local Similarity 100.0%;   Pred. No.0;
Matches 5271;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy      1 ATCTTTGTTCAGTTACCTCAGGCTATTAGGATAATGAGATAACCAATGTGAAAG  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATCTTTGTTCAGTTACCTCAGGCTATTAGGATAATGAGATAACCAATGTGAAAG  60

Qy     61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTGGCAGGATGATAAAGAATCA  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTGGCAGGATGATAAAGAATCA  120

Qy    121 GGAAGAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTAGTGA  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGAAGAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTAGTGA  180

Qy    181 CAGATGTTGCTCCTGACAGAGAACATCTTCCTCAGGAAACATCCAATATGTAAATC  240
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Db    181 CAGATGTTGCTCCTGACAGAGAACATCTTCCTCAGGAAACATCCAATATGTAAATC  240

Qy    241 CATCAAACAGGAGCTAAGAAACAGGAGATGAGATGGGCACTTGCCCAAGGAAAATGCCAG  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CATCAAACAGGAGCTAAGAAACAGGAGATGAGATGGGCACTTGCCCAAGGAAAATGCCAG  300

Qy    301 GAGAGCAAATAATGATGAAAATCAATGAATAAGGAAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAGAGCAAATAATGATGAAAATCAATGAATAAGGAAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG  360

Qy    361 ATGAGGACCAAAATCAATGAATAAGGAAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAGGACCAAAATCAATGAATAAGGAAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG  420

Qy    421 TAATTAAGTAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAATGGGAA  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TAATTAAGTAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAATGGGAA  480

Qy    481 AAACGTCAAAAGCATGATCGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT  540
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Db    481 AAACGTCAAAAGCATGATCGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT  540

Qy    541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC  600
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Qy   4441 CTTTGAAATTAGACCTCCTGCTGATCTTGTTTTAACATATTAATAAAAACATGTTTAAA  4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 CTTTGAAATTAGACCTCCTGCTGATCTTGTTTTAACATATTAATAAAAACATGTTTAAA  4500

Qy   4501 ATTTGATATTTGATAATCATTATCATTTGTTCCTTGTTCCTTTGTAATCTATATTTT  4560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 ATTTGATATTTGATAATCATTATCATTTGTTCCTTGTTCCTTTGTAATCTATATTTT  4560

Qy   4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTCCCCAGATTCACCAATGAGGTTCTTGG  4620
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Db   4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTCCCCAGATTCACCAATGAGGTTCTTGG  4620

Qy   4621 CATGCACACACAGAGAGTAAGAACTGATTTAGAGGCTAACATTGGTCGCCTGAGA  4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 CATGCACACACAGAGAGTAAGAACTGATTTAGAGGCTAACATTGGTCGCCTGAGA  4680

Qy   4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTGTGTTTAAAGTGTAGGGGTG  4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTGTGTTTAAAGTGTAGGGGTG  4740

Qy   4741 AGGGGGAAATCTGCCGCTTCTATAGGAATGCTTCTCCCTGGAGCCTGGTAGGGTGCTGTGTC  4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 AGGGGGAAATCTGCCGCTTCTATAGGAATGCTTCTCCCTGGAGCCTGGTAGGGTGCTGTGTC  4800

Qy   4801 CTTGTGTTCTGGCTGGCTGTTATTTTCTCTGTCCCTCTAGTCTTAAAGGACTTGTTT  4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 CTTGTGTTCTGGCTGGCTGTTATTTTCTCTGTCCCTCTAGTCTTAAAGGACTTGTTT  4860

Qy   4861 GGATCTTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCGAGGTTCTCAATGAGTTTGCAGAG  4920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 GGATCTTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCGAGGTTCTCAATGAGTTTGCAGAG  4920

Qy   4921 TGAATGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCAGCACCAGTAGTCCTGG  4980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 TGAATGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCAGCACCAGTAGTCCTGG  4980

Qy   4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA  5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA  5040

Qy   5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTCTTCTTTTAAAAGAAACTC  5100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTCTTCTTTTAAAAGAAACTC  5100

Qy   5101 CAAACAGACTTCTGGAAGTTATTTCTAAGAATCTTTGCTGCGAAGGTGAAGGTGAAGGCAACCCC  5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 CAAACAGACTTCTGGAAGTTATTTCTAAGAATCTTTGCTGCGAAGGTGAAGGTGAAGGCAACCCC  5160

Qy   5161 CCTGTGCAGCGCCCACCAGCCTCAGTGGCCACCTCGTCTTCCCCCATGAAGGGCTG  5220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 CCTGTGCAGCGCCCACCAGCCTCAGTGGCCACCTCGTCTTCCCCCATGAAGGGCTG  5220

Qy   5221 GCTCCCCAGTATATATAAACCTCTGGAGCTCGGGCATGAGCCAGCAAGG  5271
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Db   5221 GCTCCCCAGTATATATAAACCTCTGGAGCTCGGGCATGAGCCAGCAAGG  5271
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RESULT 3
US-08-938-669-3
; Sequence 3, Application US/08938669
;  GENERAL INFORMATION:
;    APPLICANT: Nguyen, Thai D.
;    APPLICANT: Polansky, Jon R.
;    TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
;    TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND RELATED DISEASE
;    NUMBER OF SEQUENCES: 32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Howrey & Simon
;      STREET: 1299 Pennsylvania Avenue, N.W.
;      CITY: Washington
;      STATE: DC
```

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Qy  1681  CACTGTCCTCATCACTTTCTCCCTCATCCTCATTTTCAGGCTAGTAGTTACCATTTTATT  1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  CACTGGTCCTCATCACTTTCTCCCTCATCCTCATTTTCAGGCTAGTAGTTACCATTTTATT  1740

Qy  1741  CACCATTGCTTTGTGTGTGTGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATTAG  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||||
Db  1741  CACCATGCTTTGTGTGTGTGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG  1800

Qy  1801  TTCCATTTGGGCCATCTGTGTGTATAGGGAGGAGGGCATACCCCAGAGACTCCT  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  TTCCATTTGGGCCATCTGTGTGTATAGGGAGGAGGGCATACCCCAGAGACTCCT  1860

Qy  1861  TGAAGCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGAGCCCTGCAAGCACCCGGGTCC  1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  TGAAGCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGAGCCCTGCAAGCACCCGGGTCC  1920

Qy  1921  TGGGGTGTCTGAGCAACCTGCAGCCCGTGCCACTCGTTGTTTGTTATCACTTCTCTAGG  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  TGGGTGTCTGAGCAACCTGCAGCCCGTGCCACTCGTTGTTTGTTATCACTTCTCTAGG  1980

Qy  1981  GACCTGTTGCTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  GACCTGTGCTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT  2040

Qy  2041  TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC  2100

Qy  2101  CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGAGAAATAATAGCCA  2160
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGAGAAAATAATAGCCA  2160

Qy  2161  GCCAACTTAAACCCAGTGCTGAAAGGAAATAAACACCATTCTTGAAGAATTGTGCGC  2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GCCAACTTAAACCCAGTGCTGAAAGGAAATAAACACCATTCTTGAAGAATTGTGCGC  2220

Qy  2221  AGCATCCCTTAACAAGGCCACCTCCCTAGCCCTCCTCCCTGCTGCCTCGTGCCCGCCGAGG  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  AGCATCCCTTAACAAGGCCACCTCCCTAGCCCTCCTCCCTGCTGCCTCGTGCCCGCCGAGG  2280

Qy  2281  CCCCCAAGCCCGAGTCTTCCAAGCCTTCCATCAGTCACAGCCGCTGCAGCTGGCCT  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  CCCCCAAGCCCGAGTCTTCCAAGCCTTCCATCAGTCACAGCCGCTGCAGCTGGCCT  2340

Qy  2341  GCCTCGCTTCCCGTGAATCGTTCCTGGTCATCGTCCTGGTCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT  2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  GCCTCGCTTCCCGTGAATCGTTCCTGGTCATCGTCCTGGTCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT  2400

Qy  2401  CCAGAAAGGAAATGGAGAGGGAAACTAGTCTTAACGAGGAATCTGGAGGGGGACCAGAGTGTTTC  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  CCAGAAAGGAAATGGAGAGGGAAACTAGTCTTAACGAGGAATCTGGAGGGGGACCAGAGTGTTTC  2460

Qy  2461  CTCAGAGGACGCTGGGGCTGAGCGGCTGGGACTGCAGGGAG  2520
          |||||||||||||||||||||||||||||||||||||||||
Db  2461  CTCAGAGGACGCTGGGGCTGAGCGGCTGGGACTGCAGGGAG  2520

Qy  2521  TGGGGACGCTGGGGCTGAGCGGTGTTGTGTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGTGAGC  2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  TGGGGACGCTGGGGCTGAGCGGTGTTGTGTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGTGAGC  2580

Qy  2581  GCTGCCCAGATGTTCAGTGTTCAGTGTTGTTCACGGGAGGAAGAGTCTATTCATGAAGGGGATGCAGTTTC  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  GCTGCCCAGATGTTCAGTGTTCAGTGTTGTTCACGGGAGGAAGAGTCTATTCATGAAGGGGATGCAGTTTC  2640

Qy  2641  CTTTTTATCTTTTCTCTTGATTTTCTCTGGAGGAGGAAGAGTCTATTTCATGAAGGGGATGCTGA  2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  CTTTTTATCTTTTCTCTTGATTTTCTCTGGAGGAGGAAGAGTCTATTTCATGAAGGGGATGCTGA  2700

Qy  2701  ATAAAGTCAGCTGTTAAAATTCCAGGTGTGCATGGGGTTTCTTCACGAAGGCCTTTAT  2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  ATAAAGTCAGCTGTTAAAATTCCAGGTGTGCATGGGGTTTCTTCACGAAGGCCTTTAT  2760

Qy  2761  TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCGTTAATTCACGGAAGAGTCAC  2820
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Qy   601  AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAATGGGGACTGGGAAAGCTTTCATAAC   660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAATGGGGACTGGGAAAGCTTTCATAAC   660

Qy   661  AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA   720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA   720

Qy   721  ATTGACTGGGCTAAGCCTGACTTTCAAGGGAAATATGAGAGCAAAACAAAA   780
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  ATTGACTGGGCTAAGCCTGACTTTCAAGGGAAATATGAGAGCAAAACAAAA   780

Qy   781  GACATGGTTAAAAGGCAACCAGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCTTCAGCA   840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GACATGGTTAAAAGGCAACCAGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCTTCAGCA   840

Qy   841  GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTCTTAAGGAATCTTAAGAAACTC   900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTCTTAAGGAATCTTAAGAAACTC   900

Qy   901  TTGAAAGATCATGAATTTTAACCATTTAAGTATATAAACAAATATGCGATGCATAATCAG   960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  TTGAAAGATCATGAATTTTAACCATTTAAGTATATAAACAAATATGCGATGCATAATCAG   960

Qy   961  TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020

Qy  1021  GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCACTCTTTTCAGAATGATC  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCACTCTTTTCAGAATGATC  1080

Qy  1081  TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATTCACAACCCAA  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATTCACAACCCAA  1140

Qy  1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGTCCATTACAAATGCCACCTCCTCC  1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGTCCATTACAAATGCCACCTCCTCC  1200

Qy  1201  TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCACTCTAGACTTCTGATCACGAGT  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCACTCTAGACTTCTGATCACGAGT  1260

Qy  1261  TACAGCCAGAGTCACAGGCCGCACGCCACGCCGCGTCCGTGAGGGTGAGGGTGAGGGTGTATGCTCTAC  1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  TACAGCCAGAGTCACAGGCCGCACGCCACGCCGCGTCCGTGAGGGTGAGGGTGAGGGTGTATGCTCTAC  1320

Qy  1321  ACCTGAGCTCACTGCAACCTGCCTCCGCTCCCGCCGCCGGCCGCTGAACTCCTGAACTCCTGAGGTTCTTG  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  ACCTGAGCTCACTGCAACCTGCCTCCGCTCCCGCCGCCGGCCGCTGAACTCCTGAACTCCTGAGGTTCTTG  1380

Qy  1381  CGCGTAGCTGGGACTACAGGCCACGCCACGCCGCGCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG  1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CGCGTAGCTGGGACTACAGGCCACGCCACGCCGCGCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG  1440

Qy  1441  GTTTCACCATATTAGCCCGGGCTGGTCTTGAACTCCTCAGGTGATCCACCCCACCTC  1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  GTTTCACCATATTAGCCCGGGCTGGTCTTGAACTCCTCAGGTGATCCACCCCACCTC  1500

Qy  1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGCCACCGCGCCCGGCCAAGGGGTCAGTGT  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGCCACCGCGCCCGGCCAAGGGGTCAGTGT  1560

Qy  1561  TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGAGGAAACAGACAAAAGCTGTGA  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGAGGAAACAGACAAAAGCTGTGA  1620

Qy  1621  TAATTTCAGGGATTCTTGGGATGGGAATGGTGCCATGGAATGTGCCTAGTCCGCCCAGAC  1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  TAATTTCAGGGATTCTTGGGATGGGAATGGTGCCATGGAATGTGCCTAGTCCGCCCAGAC  1680
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Db   361  ATGAGGACCAAAATCAATGATAAGGAAAACAGCTCAGAAAAAAAGATGTTTCCAAATTGG   420

Qy   421  TAATTAAGTATTTGTTCCTTGGGAAGAGAGACCTTCCATGTGAGCTTGATGGGAAATGGGAA   480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  TAATTAAGTATTTGTTCCTTGGGAAGAGAGACCTTCCATGTGAGCTTGATGGGAAATGGGAA   480

Qy   481  AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTAAAAACCAGAT   540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTAAAAACCAGAT   540

Qy   541  GGCATCACTCTGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGACATAACAATAAC   600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GGCATCACTCTGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC   600

Qy   601  AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGACTGGGAAAGCTTTCATAAC   660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGACTGGGAAAGCTTTCATAAC   660

Qy   661  AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCGTCTATACCAGGGAACACAAAA   720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCGTCTATACCAGGGAACACAAAA   720

Qy   721  ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAAATGAAAAACTGAGAGCAAAACAAAA   780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAAATGAAAAACTGAGAGCAAAACAAAA   780

Qy   781  GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA   840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA   840

Qy   841  GGGACCCTGAGCATTGCCTTTAGGAAGGCCAGTTTTCTTAGGAATCTTAAGAAACTC   900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  GGGACCCTGAGCATTGCCTTTAGGAAGGCCAGTTTTCTTAGGAATCTTAAGAAACTC   900

Qy   901  TTGAAAGATCATGAATTTAACCATTTTAAGTATAAAACAAATATGGATGCATAATCAG   960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  TTGAAAGATCATGAATTTAACCATTTTAAGTATAAAACAAATATGGATGCATAATCAG   960

Qy   961  TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC   1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC   1020

Qy  1021  GGATAGGTCAGAAATCATTAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTCAGAATGATC   1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGATAGGTCAGAAATCATTAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTCAGAATGATC   1080

Qy  1081  TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA   1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA   1140

Qy  1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC   1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC   1200

Qy  1201  TGTGCAGCCCATCCCGCTCCAGAAGTCTCCCCACAGGAGTCCTCCCACTCTAGACTTCTG   1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  TGTGCAGCCCATCCCGCTCCAGAAGTCTCCCCACAGGAGTCCTCCCACTCTAGACTTCTG   1260

Qy  1261  TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTCTTCTTACACCTGTAAATC   1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTCTTCTTACACCTGTAAATC   1320

Qy  1321  ACCTGAGCTCACTGCAACCTGCCTTCCCAGTTCAAGCAATTCTCCGTCTCAGCCTCC   1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  ACCTGAGCTCACTGCAACCTGCCTTCCCAGTTCAAGCAATTCTCCGTCTCAGCCTCC   1380

Qy  1381  CGCGTAGCTGGGACTACAGGCGCCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG   1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CGCGTAGCTGGGACTACAGGCGCCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG   1440

Qy  1441  GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCCACCCACCTC   1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCCACCCACCTC   1500
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Qy  4981  TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA   5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4981  TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA   5040

Qy  5041  TAGGAACTATTATTGGGTATGGGTGCATAAATTGGGATGTTCTTTTAAAAGAAACTC   5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5041  TAGGAACTATTATTGGGTATGGGTGCATAAATTGGGATGTTCTTTTAAAAGAAACTC   5100

Qy  5101  CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGCAGCGTGAAGGCAACCCC   5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5101  CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGCAGCGTGAAGGCAACCCC   5160

Qy  5161  CCTGTGCACAGCCCCAGCCTACGTGCCCACCTTGCTTCCTGTCCTGTTGAAGGGGCTG   5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5161  CCTGTGCACAGCCCCAGCCTACGTGCCCACCTTGCTTCCTGTCCTGTTGAAGGGGCTG   5220

Qy  5221  GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG   5271
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5221  GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG   5271
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RESULT 4

US-09-227-881-3

; Sequence 3, Application US/09227881
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/227,881
; CURRENT FILING DATE: 1999-01-11
; EARLIER APPLICATION NUMBER: US 08/938,669
; EARLIER FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 3
; LENGTH: 6169
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-227-881-3

Query Match   100.0%;   Score 5271;   DB 22;   Length 6169;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 5271;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy     1  ATCTTTGTTCAGTTACCTCAGGGCTATTATGGCTATTGGCAGGATAACCAATGTGAAAG     60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ATCTTTGTTCAGTTACCTCAGGGCTATTATGGCTATTGGCAGGATAACCAATGTGAAAG     60

Qy    61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA    120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA    120

Qy   121  GGAAGAGGAGTATCCACGTTAGCCAGTGTCCAGGCGTGTCTGCGCTGTCTTATTTTAGTGA    180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GGAAGAGGAGTATCCACGTTAGCCAGTGTCCAGGCGTGTCTGCGCTGTCTTATTTTAGTGA    180

Qy   181  CAGATGTTGCTCCTGACAGAGAACAGGAAACAGGAATGAGATGAGAAATGAGATAACCAATGTGAAATC    240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  CAGATGTTGCTCCTGACAGAGAACAGGAAACAGGAATGAGATGAGAAATGAGATAACCAATATGGTAAATC    240

Qy   241  CATCAAAACAGGAGCTAAGAAACAGGAATGGGCACTTGCCCAAGGAAAAATGCCAG    300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  CATCAAAACAGGAGCTAAGAAACAGGAATGGGCACTTGCCCAAGGAAAAATGCCAG    300

Qy   301  GAGAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTAATTCAGGAGAAAAATG    360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  GAGAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTAATTCAGGAGAAAAATG    360

Qy   361  ATGAGGACCAAAATCAATGATAAGGAAAACAGCTCAGAAAAAAAGATGTTTCCAAATTGG    420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT  1560

Qy  1561  TTAATAAGGAATAACTTGAATGCTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  TTAATAAGGAATAACTTGAATGCTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA  1620

Qy  1621  TAATTTCAGGGATTCTTGGGATGGGAATGGTGCCATGAGTCTGCCTGCCTAGTCCCAGAC  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  TAATTTCAGGGATTCTTGGGATGGGAATGGTGCCATGAGTCTGCCTGCCTAGTCCCAGAC  1680

Qy  1681  CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGTCAAGTTACCATTTTATT  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGTCAAGTTACCATTTTATT  1740

Qy  1741  CACCATGCTTTTGTGGTAAGCCTCCACATGTTACTGAAATAAGAGTATACATAAAACTAG  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  CACCATGCTTTTGTGGTAAGCCTCCACATGTTACTGAAATAAGAGTATACATAAAACTAG  1800

Qy  1801  TTCCATTTGGGGCCATCTGTGTGTGTATAGGGAGGAGGGCATACCCCAGAGACTCCT  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  TTCCATTTGGGGCCATCTGTGTGTGTATAGGGAGGAGGGCATACCCCAGAGACTCCT  1860

Qy  1861  TGAAGCCCCGGCAGAGTTTCCTCTGCCAGCCCGTGCCACTGGGGGAGCCCTGCAAGCACCCGGGGTCC  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  TGAAGCCCCGGCAGAGTTTCCTCTGCCAGCCCGTGCCACTGGGGGAGCCCTGCAAGCACCCGGGGTCC  1920

Qy  1921  TGGGTGTTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTGTTGTTTATCACTCTCTAGG  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  TGGGTGTTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTGTTGTTTATCACTCTCTAGG  1980

Qy  1981  GACCTGTTGCTTTCTATTCTGTGTGACTCGTTCATTCATTCCAGGCATTCATTGACAATT  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  GACCTGTTGCTTTCTATTCTGTGTGACTCGTTCATTCATTCCAGGCATTCATTGACAATT  2040

Qy  2041  TATTGAGTACTTATATCTGCCAGACACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  TATTGAGTACTTATATCTGCCAGACACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC  2100

Qy  2101  CCTACCTTCGTTGGAGGTGACAGTTCTCATGGAAGACGTGCAGAAGAAATTAATAGCCA  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCTACCTTCGTTGGAGGTGACAGTTCTCATGGAAGACGTGCAGAAGAAATTAATAGCCA  2160

Qy  2161  GCCAACTTAAACCCAGTGCTGAAAGAAGAAATAAACACCATCTTGAGCTGTGTGCGC  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GCCAACTTAAACCCAGTGCTGAAAGAAGAAATAAACACCATCTTGAGCTGTGTGCGC  2220

Qy  2221  AGCATCCCTTAACAAGGCACCTCCCTAGCCGCCCCCGCCCCGTGCCTGCCTCCGTCGTGCCCGGAGG  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  AGCATCCCTTAACAAGGCACCTCCCTAGCCGCCCCCGCCCCGTGCCTGCCTCCGTCGTGCCCGGAGG  2280

Qy  2281  CCCCAAGCCCGAGTCTTCCAAGCCTCACAGCCGCTGCAGCTGCCT  2340
          |||||||||||||||||||||||||||||||||||||||||||||
Db  2281  CCCCAAGCCCGAGTCTTCCAAGCCTCACAGCCGCTGCAGCTGCCT  2340

Qy  2341  GCCTCGCTTCCCGTTCCCGTGAATCGTCCGTGGTCATCTGAGCTGAGACTCCTTGGCTCCAGGCT  2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  GCCTCGCTTCCCGTTCCCGTGAATCGTCCGTGGTCATCTGAGCTGAGACTCCTTGGCTCCAGGCT  2400

Qy  2401  CCAGAAAGGGAAATGGAGAGGGGCCTCCACGTCCAGGAGAATTCGGAGGGGACTGGGGACAGTGTTTC  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  CCAGAAAGGGAAATGGAGAGGGGCCTCCACGTCCAGGAGAATTCGGAGGGGACTGGGGACAGTGTTTC  2460

Qy  2461  CTCAGAGGGAAAGGGCTCGGGCGTGCTGAGCCGGTCGGTGGTGGGGCTGAAAAGGGCAAGGCTGAA  2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  CTCAGAGGGAAAGGGCTCGGGCGTGCTGAGCCGGTCGGTGGTGGGGCTGAAAAGGGCAAGGCTGAA  2520

Qy  2521  TGGGACGCGTCGGGCGTGCTGAGCCGGTCGGTGGGGCTGAAAAGGGCAAGGCTGAA  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  TGGGACGCGTCGGGCGTGCTGAGCCGGTCGGTGGGGCTGAAAAGGGCAAGGCTGAA  2580
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Qy  2581  GCTGCCCAGATGTTCAGTGTGTTGTTCACCGGGGCTGGGAGTTTCCGTTGCTTCCTGTGAGC  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  GCTGCCCAGATGTTCAGTGTGTTGTTCACCGGGGCTGGGAGTTTCCGTTGCTTCCTGTGAGC  2640

Qy  2641  CTTTTATCTTCTTCTCTGCTTCGGGAGGAGAGAGAGTCTATTCATGAAGGGATGCAGTTTAT  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  CTTTTATCTTCTTCTCTGCTTCGGGAGGAGAGAGAGTCTATTCATGAAGGGATGCAGTTTC  2700

Qy  2701  ATAAAGTCAGCTGTTAAAATTCAGGTGTGCATGGGTTCCTTCACGAAGGCCTTTAT  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  ATAAAGTCAGCTGTTAAAATTCAGGTGTGCATGGGTTCCTTCACGAAGGCCTTTAT  2760

Qy  2761  TTAATGGAATATAGGAAGCGAGCTCATTCCTAGGCCGTTAATTCACCGGAAGAAGTGAC  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  TTAATGGAATATAGGAAGCGAGCTCATTCCTAGGCCGTTAATTCACCGGAAGAAGTGAC  2820

Qy  2821  TGGAGTCTTTCTTCCATGTCTTCTCGGGCAACTACTCAGCCCGTGTGGGACTTGGCTTA  2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  TGGAGTCTTTCTTCCATGTCTTCTCGGGCAACTACTCAGCCCGTGTGGGACTTGGCTTA  2880

Qy  2881  TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTCTTTCGGTTCTGTTCGCCATT  2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTCTTTCGGTTCTGTTCGCCATT  2940

Qy  2941  GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTTCCCGGCCATAGTCTCTCTGCT  3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTTCCCGGCCATAGTCTCTCTGCT  3000

Qy  3001  ATAAAGACCCTTGCAGCTCCCGTGTTGTTCGTGAACACTTCCCTGTGATTCTCTGTGAGGGG  3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  ATAAAGACCCTTGCAGCTCCCGTGTTGTTCGTGAACACTTCCCTGTGATTCTCTGTGAGGGG  3060

Qy  3061  GGATGTTGAGAGGGGAAGGAGGGCAGAGCAGAAGTGGGTGCTCCATCAGTCCTCACTCAGTCACGTCAGACTC  3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  GGATGTTGAGAGGGGAAGGAGGGCAGAGCAGAAGTGGGTGCTCCATCAGTCCTCACTCAGTCACGTCAGACTC  3120

Qy  3121  GGACAGGAAGGCAGGCAGGCAGCAGAAGTGGGCAGAGATTGCCAAGAGATTG  3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  GGACAGGAAGGCAGGCAGGCAGCAGAAGTGGGCAGAGATTGCCAAGAGATTG  3180

Qy  3181  CAGGACCGAGAGCCACATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT  3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181  CAGGACCGAGAGCCACATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT  3240

Qy  3241  TCCCTAAGCATAGACAATGGCCAATAACCAAAAGAAATGCAGAGACTAACTGT  3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  TCCCTAAGCATAGACAATGGCCAATAACCAAAAGAAATGCAGAGACTAACTGT  3300

Qy  3301  GGTAGCTTTGGCTGGCATTCAAAAACTGGGCATCAAAAATGTGAAAATGCCAGAGATTG  3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301  GGTAGCTTTGGCTGGCATTCAAAAACTGGGCATCAAAAATGTGAAAATGCCAGAGATTG  3360

Qy  3361  TTAAACTTTTCACCCTGACCACGCAGCCGTCACAGCCTTGTGGGGGAAAAATCAGTTCCT  3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361  TTAAACTTTTCACCCTGACCACGCAGCCGTCACAGCCTTGTGGGGGAAAAATCAGTTCCT  3420

Qy  3421  AGTGACCTGCACAATGCATTGGCGCCAATAACCAAATAACCAGAGAGGGGATAGTGTATGAGCAAGAAAG  3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421  AGTGACCTGCACAATGCATTGGCGCCAATAACCAAATAACCAGAGAGGGGATAGTGTATGAGCAAGAAAG  3480

Qy  3481  ACAGATTCATTCAAGGCAGTGGAATTGACCACAGGGATTATAGTCCACGGTGATCCTGG  3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481  ACAGATTCATTCAAGGCAGTGGAATTGACCACAGGGATTATAGTCCACGGTGATCCTGG  3540

Qy  3541  GTTCTAGGAGGCAGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAAGTCGGAGA  3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541  GTTCTAGGAGGCAGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAAGTCGGAGA  3600

Qy  3601  CCTGATTTCTAATACTATATTTTCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG  3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601  CCTGATTTCTAATACTATATTTTCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG  3660

Qy  3661  GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTCTCTGT  3720
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Thu Jan 26 14:20:40 2006

2006

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Db    3661 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTTCCTTATTAGCAGAGAAGAAACATTCTTTTTCTCTGT 3720

Qy    3721 GGAGTTAGCAGCAGCAAGGGCAATCCCGTTCTTCGTTCTTTTCTTTAACAGGAGAAGAAAAACATTCCTTAAGAG 3780
Db    3721 GGAGTTAGCAGCAGCAAGGGCAATCCCGTTCTTCGTTCTTTTCTTTAACAGGAGAAGAAAAACATTCCTTAAGAG 3780

Db    3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAT 3840
Qy    3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAT 3840

Qy    3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db    3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

Qy    3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
Db    3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960

Qy    3961 AGAATAGAATCTTAGAGCAAACTGTCTTCACAAGTATTGACACTGTTGTGTATTGGTATAAAGT 4020
Db    3961 AGAATAGAATCTTAGAGCAAACTGTCTTCACAAGTATTGACACTGTTGTGTATTGGTATAAAGT 4020

Qy    4021 AGTTTGGAAATATTTCAAGTGGCTTAAAGTACTTCTGACAGTTTTGGTATAT 4080
Db    4021 AGTTTGGAAATATTTCAAGTGGCTTAAAGTACTTCTGACAGTTTTGGTATAT 4080

Qy    4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTACTTCTGACAGTTTTGGTATAT 4140
Db    4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTACTTCTGACAGTTTTGGTATAT 4140

Qy    4141 TTATTGGCTATTGCCATTGCTTTTTGTTTTTGTTTTTCTCTTTGTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
Db    4141 TTATTGGCTATTGCCATTGCTTTTTGTTTTTGTTTTTCTCTTTGTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200

Qy    4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGAGAAAAAATTACATTTT 4260
Db    4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGAGAAAAAATTACATTTT 4260

Qy    4261 TGTTTTTTACCACCTTCTAACTAAATTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
Db    4261 TGTTTTTTACCACCTTCTAACTAAATTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320

Qy    4321 CTCAAAGTGGTAATAACAGTACCTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
Db    4321 CTCAAAGTGGTAATAACAGTACCTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380

Qy    4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGTAAGTGTGAAATATTTATACTTCAAAACTA 4440
Db    4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGTAAGTGTGAAATATTTATACTTCAAAACTA 4440

Qy    4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500
Db    4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500

Qy    4501 ATTTTGATATTTTGATAATCATATTTGTTTCCTTTGTAATCTATATTTT 4560
Db    4501 ATTTTGATATTTTGATAATCATATTTGTTTCCTTTGTAATCTATATTTT 4560

Qy    4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620
Db    4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620

Db    4621 CATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680
Qy    4621 CATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680

Qy    4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGGTG 4740
Db    4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGGTG 4740

Qy    4741 AGGGGGGAAATCTGCCGCTTCATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800
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Db    4741 AGGGGGGAAATCTGCCGCTTCATAGGAATGCTCTCCCTGCTACGTCTTAAAGACTTGTTT 4800
Qy    4801 CTTGTGTTCTCGGCTGGCTGGTGTTATTTTCTCTGTCCCTGCTACGTCTTAAAGACTTGTTT 4860
Db    4801 CTTGTGTTCTCGGCTGGCTGGTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGACTTGTTT 4860

Qy    4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGTTCTCAATGAGTTGCAGAG 4920
Db    4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGTTCTCAATGAGTTGCAGAG 4920

Qy    4921 TGAATGAAATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980
Db    4921 TGAATGAAATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980

Qy    4981 TGTAAGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGTGTGGAGATA 5040
Db    4981 TGTAAGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGTGTGGAGATA 5040

Qy    5041 TAGGAACTATTATTGGGTGCATAAATTGGGATGTTCTTTTTAAAAGAAACTC 5100
Db    5041 TAGGAACTATTATTGGGTGCATAAATTGGGATGTTCTTTTTAAAAGAAACTC 5100

Qy    5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTCGGCAGCGTGAAGGCAACCCC 5160
Db    5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTCGGCAGCGTGAAGGCAACCCC 5160

Qy    5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCGTCTTCCCCATGAAGGGCTG 5220
Db    5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCGTCTTCCCCATGAAGGGCTG 5220

Qy    5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGCAGCATGAGCCAGCAAGG 5271
Db    5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGCAGCATGAGCCAGCAAGG 5271
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RESULT 5
US-10-244-633-3
; Sequence 3, Application US/10244633
; GENERAL INFORMATION:
;   APPLICANT: Nguyen, Thai D.
;   APPLICANT: Polansky, Jon R.
;   APPLICANT: Chen, Pu
;   APPLICANT: Chen, Hua
;   TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
;   TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
;   TITLE OF INVENTION: Disorders
;   FILE REFERENCE: 07425.0057.US01
;   CURRENT APPLICATION NUMBER: US/10/244,633
;   CURRENT FILING DATE: 2002-09-17
;   PRIOR APPLICATION NUMBER: US/09/306,828
;   PRIOR FILING DATE: 1999-05-07
;   PRIOR APPLICATION NUMBER: US 09/227,881
;   PRIOR FILING DATE: 1999-01-11
;   NUMBER OF SEQ ID NOS: 38
;   SOFTWARE: Microsoft Word 97
;   SEQ ID NO 3
;   LENGTH: 6169
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-244-633-3

Query Match   100.0%; Score 5271; DB 43; Length 6169;
Best Local Similarity 100.0%;
Matches 5271; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    1 ATCTTTGTTCAGTTACCTCAGGGCTATTACAGGGCTATTATGAAATGAAATGAGATAACCAATGAAATGTGAAAG 60
Db    1 ATCTTTGTTCAGTTACCTCAGGGCTATTACAGGGCTATTATGAAATGAAATGAGATAACCAATGAAATGTGAAAG 60

Qy   61 TCCTATAAACTGTATAGCCTTCATTCGATGTATGTCTTGCAGGATGTATGTCTTGCAGGATGATAAAGAATCA 120
Db   61 TCCTATAAACTGTATAGCCTTCATTCGATGTATGTCTTGCAGGATGTATGTCTTGCAGGATGATAAAGAATCA 120
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Qy    121 GGAAGAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTAGTGA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGAAGAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTAGTGA 180

Qy    181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy    241 CATCAAACAGAGCTAAGAAACAGGAATGAGAATGAGAAATGGGCACTTGCCCAAGGAAATGCCAG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CATCAAACAGAGCTAAGAAACAGGAATGAGAATGAGAAATGGGCACTTGCCCAAGGAAATGCCAG 300

Qy    301 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTAATTTCAGGAAAAAATG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTAATTTCAGGAAAAAATG 360

Qy    361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy    421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGTGGGAAAATGGGAA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGTGGGAAAATGGGAA 480

Qy    481 AAACGTCAAAGCCATGCAGATCTGATCAGATCCCAAAGTGCCAAAGTGCCAAAGTCTTTCATAAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAACGTCAAAGCCATGCAGATCTGATCAGATCCCAAAGTGCCAAAGTGCCAAAGTCTTTCATAAC 540

Qy    541 GGCATCACTCTGGGGAGCAAGTTCAGGAAGTTCATGTTAGCAAGGACATACAATAAAC 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGCATCACTCTGGGGAGCAAGTTCAGGAAGTTCATGTTAGCAAGGACATACAATAAAC 600

Qy    601 AGCAAAATCAAAATTCCGCAGAAGCAGAGAGAAATGGGACTTTCATTCATTCAGTAAAC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCAAAATCAAAATTCCGCAGAAGCAGAGAGAAATGGGACTTTCATTCATTCAGTAAAC 660

Qy    661 AGTGATTAGGCAGTTGCCTTTAGGAAGGCCATTTGCCTTTAGGAAGGCCAGTTTCTTAGGAAGGCCAGTTTCTT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGTGATTAGGCAGTTGCCTTTAGGAAGGCCATTTGCCTTTAGGAAGGCCAGTTTCTTAGGAAGGCCAGTTTCTT 720

Qy    721 ATTGACTGGGCTAAGCCTGACTTTCAAGGGAAATATGAGAGACAAAACAAAA 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATTGACTGGGCTAAGCCTGACTTTCAAGGGAAATATGAGAGACAAAACAAAA 780

Qy    781 GACATGGTTAAAAGGCAACCAACATTGTGAGCCTTCAAAGCTGAGCCCCTCAGCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GACATGGTTAAAAGGCAACCAACATTGTGAGCCTTCAAAGCTGAGCCCCTCAGCA 840

Qy    841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 900

Qy    901 TTGAAAGATCATGAATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TTGAAAGATCATGAATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy    961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATCAAATGCCACCGTGTCCCAGCTCC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATCAAATGCCACCGTGTCCCAGCTCC 1020

Qy   1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTCAGAATGATC 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTCAGAATGATC 1080

Qy   1081 TGTCATAGCCCTCACACACAGCCCGATGTGTCTGACCTACAACCACATCCTACAACCCAA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTCATAGCCCTCACACACAGCCCGATGTGTCTGACCTACAACCACATCCTACAACCCAA 1140

Qy   1141 GTGCCTCAACCATTGTTAACGTGTCATCTCCAGTAGTTCCCATTACAAATGCCACCGTC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GTGCCTCAACCATTGTTAACGTGTCATCTCCAGTAGTTCCCATTACAAATGCCACCGTC 1200

Qy   1201 GTGTGCAGCCCCATCCCGCTTCCACAGGAAGTCTTCCCACTGTACTTCTCTGCATCACGATGT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GTGTGCAGCCCCATCCCGCTTCCACAGGAAGTCTTCCCACTGTACTTCTCTGCATCACGATGT 1260
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Db   1201 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          TGTGCAGCCCGCCATCCGCTTCCACAGGAAGTCTTCCCACTGTACTTCTCTGCATCACGATGT 1260

Qy   1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTCTCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCTAC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTCTCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCTAC 1320

Qy   1321 ACCTGAGCTCACTGCAACCTCTGCCTCCTGCCTCTGCCTCTGCCTCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ACCTGAGCTCACTGCAACCTCTGCCTCCTGCCTCTGCCTCTGCCTCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy   1381 CGGGTAGCTGGGACTACAGGCGCACGCCACCGCCCGGCTAATTTTGTATTGTTAGTAGAGATGGG 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CGGGTAGCTGGGACTACAGGCGCACGCCACCGCCCGGCTAATTTTGTATTGTTAGTAGAGATGGG 1440

Qy   1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy   1501 AGCCTCCTAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCCAAGGGTCAGTGT 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGCCTCCTAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCCAAGGGTCAGTGT 1560

Qy   1561 TTAATAAGGAATAACTTGAATGGTTTACTCAAACACAGGGAAACAGACAAAAGCTGTGA 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TTAATAAGGAATAACTTGAATGGTTTACTCAAACACAGGGAAACAGACAAAAGCTGTGA 1620

Qy   1621 TAATTCAGGGATTCTTGGGATGGGAATGGGATGGGCCATGAGCTGCCTGCCCTAGTCCCAGAC 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TAATTCAGGGATTCTTGGGATGGGAATGGGATGGGCCATGAGCTGCCTGCCCTAGTCCCAGAC 1680

Qy   1681 CACTGGTCCTCATCACTTTCTTCTCCCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CACTGGTCCTCATCACTTTCTTCTCCCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy   1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAAATAAGAGTATACATAAACTAG 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAAATAAGAGTATACATAAACTAG 1800

Qy   1801 TTCCATTTGGGCCATCTGTGTGTGTGTGTGTATAGGGGGAGGGGCATACCCCAGACTCCT 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 TTCCATTTGGGCCATCTGTGTGTGTGTGTGTATAGGGGGAGGGGCATACCCCAGACTCCT 1860

Qy   1861 TGAAGCCCCGGCGAGAGTTTCTCTCGCAGCTGGGGGAGCCCCTGCAAGCACCCGGGGTCC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TGAAGCCCCGGCGAGAGTTTCTCTCGCAGCTGGGGGAGCCCCTGCAAGCACCCGGGGTCC 1920

Qy   1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTGTTTGTTATCTCTCTAGG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTGTTTGTTATCTCTCTAGG 1980

Qy   1981 GACCTGGTCTTCATTTCTGTGTGACTCGTTCATTCATCAGGCATTCATTCATTGACAATT 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 GACCTGGTCTTCATTTCTGTGTGACTCGTTCATTCATCAGGCATTCATTCATTGACAATT 2040

Qy   2041 TATTGTAGACTTATATCTGCCAGACACCAGAGACACCAGAAGACGTGAGCAGTCACTGC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TATTGTAGACTTATATCTGCCAGACACCAGAGACACCAGAAGACGTGAGCAGTCACTGC 2100

Qy   2101 CCTACCTTCGTGGAGTGACAGTTTCTCATGGAAGACGTTTCTCATGGAAGAGAAAATAATAGCCA 2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCTACCTTCGTGGAGTGACAGTTTCTCATGGAAGACGTTTCTCATGGAAGAGAAAATAATAGCCA 2160

Qy   2161 GCCAACTTAAACCCAGTGCTACAACCCGTGCTACAACCATCTTGAAGAATTGTGCGC 2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GCCAACTTAAACCCAGTGCTACAACCCGTGCTACAACCATCTTGAAGAATTGTGCGC 2220

Qy   2221 AGCATCCCTTAACAAGGCCACCTCCTAGCGCCCCTGCTCCGTGCCCGAGG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 AGCATCCCTTAACAAGGCCACCTCCTAGCGCCCCTGCTCCGTGCCCGAGG 2280

Qy   2281 CCCCCAAGCCCGAGTCTTCCACAGGAAGTCTTCCCACTGTACTTCTCTGCATCACGATGT 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CCCCCAAGCCCGAGTCTTCCACAGGAAGTCTTCCCACTGTACTTCTCTGCATCACGATGT 2340
```

Db   2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCCAGTCACAGCGCTGCAGCTGGCCT 2340

Qy   2341 GCCTCGCTTCCCGTGAATCGTCCTGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 GCCTCGCTTCCCGTGAATCGTCCTGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy   2401 CCAGAAAGGAAATGGAGAGGGAAAACTAGTCTAACGGAAATCTGGAGGGGACAGTGTTTC 2460
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 CCAGAAAGGAAATGGAGAGGGAAAACTAGTCTAACGGAAATCTGGAGGGGACAGTGTTTC 2460

Qy   2461 CTCAGAGGGAAAGGGGCCTTCCACGTCCAGAGAATTCCAGGAGGTGGGACTGCAGGGAG 2520
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CTCAGAGGGAAAGGGGCCTTCCACGTCCAGAGAATTCCAGGAGGTGGGACTGCAGGGAG 2520

Qy   2521 TGGGGACGCTGGGGGCTGAGCCGGCTGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGCAAGGCTGAA 2580
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TGGGGACGCTGGGGGCTGAGCCGGCTGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGCAAGGCTGAA 2580

Qy   2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTCCGTTGCTTCCTGTGAGC 2640
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTCCGTTGCTTCCTGTGAGC 2640

Qy   2641 CTTTTTATCTTTTCTCTGCTTGGAGGAAGAAGTCTATTCATGAAGGGATGACGTCAGTTTC 2700
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 CTTTTTATCTTTTCTCTGCTTGGAGGAAGAAGTCTATTCATGAAGGGATGACGTCAGTTTC 2700

Qy   2701 ATAAAGTCAGCTGTGTTAAAATTCCAGGGTGTGATGGGTTTTCCTTCACGGAGGCCTTTAT 2760
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 ATAAAGTCAGCTGTGTTAAAATTCCAGGGTGTGATGGGTTTTCCTTCACGGAGGCCTTTAT 2760

Qy   2761 TTAATGGGAATATAGGAAGCCAGCTCATTTCCTAGGCCGTTAATTCCACGGAAGAAGTGAC 2820
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TTAATGGGAATATAGGAAGCCAGCTCATTTCCTAGGCCGTTAATTCCACGGAAGAAGTGAC 2820

Qy   2821 TGGAGTCTTTTCTTCTCTGCAACTACTCAGCCCTGTCGTCGTGACTTGGCTTA 2880
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TGGAGTCTTTTCTTCTCTGCAACTACTCAGCCCTGTCGTCGTGACTTGGCTTA 2880

Qy   2881 TGCAAGACGGTCGAAAACCTTGGAATCGAGAGACTCGGTTTTTCTTCGGTTCTGGTTCTGCATT 2940
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 TGCAAGACGGTCGAAAACCTTGGAATCGAGAGACTCGGTTTTTCTTCGGTTCTGGTTCTGCATT 2940

Qy   2941 GGTTGGCTGTGCGACCGGTGGCAAGTGTCTCTCCTTCCTTCCTGGGCCATAGTCTTCTCTGCT 3000
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 GGTTGGCTGTGCGACCGGTGGCAAGTGTCTCTCCTTCCTTCCTGGGCCATAGTCTTCTCTGCT 3000

Qy   3001 ATAAAGACCCCTGCAGCTCTCTCGTGTTCTGTGAACACTTCCCGTGATTCTGTGAGGGGG 3060
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 ATAAAGACCCCTGCAGCTCTCTCGTGTTCTGTGAACACTTCCCGTGATTCTGTGAGGGGG 3060

Qy   3061 GGATGTGTGAGAGGGGAGGAGGAGCAGCAGAGCTGGGTGCTCCATCAGTCCAGAAAGCCTGAAATTGAGAATTGAAATTACATTTT 3120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 GGATGTGTGAGAGGGGAGGAGGAGCAGCAGAGCTGGGTGCTCCATCAGTCCAGAAAGCCTGAAATTGAGAATTGAAATTACATTTT 3120

Qy   3121 GGACAGGAAGGCAGGCAGGCAGAAGCTGGGGTGTCTCCAATCCAGTGGGTTATTGGGTTATTGGGTTATTAATGGAACCCATAAA 3180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGACAGGAAGGCAGGCAGGCAGAAGCTGGGGTGTCTCCAATCCAGTGGGTTATTGGGTTATTGGGTTATTAATGGAACCCATAAA 3180

Qy   3181 CAGGACCGAGAGCCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACACCACACATTTTCCT 3240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CAGGACCGAGAGCCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACACCACACATTTTCCT 3240

Qy   3241 TCCCTAAGCATAGACAATAGACTACGTTCAATTTGCCAATAACCAAAAGAATGCAGAGACTAACTGGT 3300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TCCCTAAGCATAGACAATAGACTACGTTCAATTTGCCAATAACCAAAAGAATGCAGAGACTAACTGGT 3300

Qy   3301 GGTAGCTTTGCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GGTAGCTTTGCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360

Qy   3361 TTAAACTTTTCACCCTGACCAGCACCCCACCCCCACGCAGCTGCAGCTGCTGACTGGACAGCACACGG 3420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TTAAACTTTTCACCCTGACCAGCACCCCACCCCCACGCAGCTGCAGCTGCTGACTGGACAGCACACGG 3420

Qy   3421 AGTGACCTGAGCGCAGCGCCAGGGGAGGGGAGGAGAGAAAAGAGAGGGGATAGTGTATGAGCAAGAAAG 3480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGTGACCTGAGCGCAGCGCCAGGGGAGGGGAGGAGAGAAAAGAGAGGGGATAGTGTATGAGCAAGAAAG 3480

Qy   3481 ACAGATTCATTCAAGGGCAGTGGAATTGACCACCAGGGATTATAGTCCACGTGATCCTGG 3540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 ACAGATTCATTCAAGGGCAGTGGAATTGACCACCAGGGATTATAGTCCACGTGATCCTGG 3540

Qy   3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGAAAAATCAGTTCAAGGAAGTCGGGAGA 3600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGAAAAATCAGTTCAAGGAAGTCGGGAGA 3600

Qy   3601 CCTGATTTCTAATACTATATTTTCCTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 CCTGATTTCTAATACTATATTTTCCTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660

Qy   3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAGAACTCTTTTTCTCTGT 3720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAGAACTCTTTTTCTCTGT 3720

Qy   3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTCTTTTAACAGGAAGAAAACATTCCTAGAG 3780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTCTTTTAACAGGAAGAAAACATTCCTAGAG 3780

Qy   3781 TAAAGCCAAACAGATTCAAGGCCTAGGTTTTCCTTCACGGAGGCCTTTAT 3840
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TAAAGCCAAACAGATTCAAGGCCTAGGTTTTCCTTCACGGAGGCCTTTAT 3840

Qy   3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

Qy   3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGCTTAACTGCAGAACCAATCAAAA 3960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGCTTAACTGCAGAACCAATCAAAA 3960

Qy   3961 AGAATAGAAATCTTTAGAGCAAACTGTGTTCTTCCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 AGAATAGAAATCTTTAGAGCAAACTGTGTTCTTCCCACATCTGGAGGTGAGTCTGCCAGGGC 4020

Qy   4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTGTATTAACACATAAAGT 4080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTGTATTAACACATAAAGT 4080

Qy   4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTAAAGTTCTGACAGTTTTGGTATAT 4140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTAAAGTTCTGACAGTTTTGGTATAT 4140

Qy   4141 TTATTGCTATTGCCATTTGCCATTTGCTTTTTGTTTTTCTCTTGGGTTATTAATGTAAAGCAG 4200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 TTATTGCTATTGCCATTTGCCATTTGCTTTTTGTTTTTCTCTTGGGTTATTAATGTAAAGCAG 4200

Qy   4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTGAATGAGGAAAAATTACATTTT 4260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTGAATGAGGAAAAATTACATTTT 4260

Qy   4261 TGTTTTTACCACTTCAACTAAATTTATTCATTTCCATTGCAATAGAGCCCATAAA 4320
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 TGTTTTTACCACTTCAACTAAATTTATTCATTTCCATTGCAATAGAGCCCATAAA 4320

Qy   4321 CTCAAAGTGTAATAACAGTACCGTGATTTTGTCATTACCAATAGAATCACAGACATT 4380
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 CTCAAAGTGTAATAACAGTACCGTGATTTTGTCATTACCAATAGAATCACAGACATT 4380

Qy   4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTTCAAAACTA 4440
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTTCAAAACTA 4440

Qy   4441 CTTTGAAATTAGACCTCCGTCTGGATCTTGTTTTTGTTTTAATAAAACATGTTTAAA 4500
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 CTTTGAAATTAGACCTCCGTCTGGATCTTGTTTTTTAACATATTTAATAAAACATGTTTAAA 4500

```
OPERATING SYSTEM:   DOS
SOFTWARE:   FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER:  US/08/938,669
  FILING DATE:
  CLASSIFICATION:  435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER:  08/791,154
  FILING DATE:  28-JAN-1997
ATTORNEY/AGENT INFORMATION:
  NAME:  Sira, Serge
  REGISTRATION NUMBER:  39,445
  REFERENCE/DOCKET NUMBER:  07425-0034
TELECOMMUNICATION INFORMATION:
  TELEPHONE:  202 383-6857
  TELEFAX:  202 383-6610
  TELEX:
INFORMATION FOR SEQ ID NO:  1:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  5300 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear

US-08-938-669-1

Query Match         99.5%;   Score 5246.4;   DB 19;  Length 5300;
Best Local Similarity  99.9%;   Pred. No. 0;
Matches 5269;   Conservative  0;  Mismatches  1;  Indels  2;  Gaps  2;

Qy      1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAAATGAGATAACCAATGTGAAAG    60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAAATGAGATAACCAATGTGAAAG    60

Qy     61 TCCTATAAACTGTATAGCCTCATTCGGATGTATGTCTTGGCAGGATGATGATAAAGAATCA   120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCTATAAACTGTATAGCCTCATTCGGATGTATGTCTTGGCAGGATGATGATAAAGAATCA   120

Qy    121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTCGTGCTCCTATTTTAGTGA   180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTCGTGCTCCTATTTTAGTGA   180

Qy    181 CAGATGTTGCTCCTGACAGAAGTATTCTTCAGGAAGAACATCACATCCAATATGTGTAAATC   240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CAGATGTTGCTCCTGACAGAAGTATTCTTCAGGAAGAACATCACATCCAATATGTGTAAATC   240

Qy    241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGAGAATGAGAAATGCCAG   300
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGAGAATGAGAAATGCCAG   300

Qy    301 GAGAGCAAATAATGATGAAAATAAACTTTCCCTTTGTTTTTAATTTCAGGAAAAAAATG   360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAGAGCAAATAATGATGAAAATAAACTTTCCCTTTGTTTTTAATTTCAGGAAAAAAATG   360

Qy    361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAGATGTTTCCAAATTGG   420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAGATGTTTCCAAATTGG   420

Qy    421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTTCCATGTGAGCTTGATGGGAAATGGGAA   480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTTCCATGTGAGCTTGATGGGAAATGGGAA   480

Qy    481 AAACGTCAAAAGCATGGTCAAAAGTGGATTATTTTAAAAACCAGAT   540
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAACGTCAAAAGCATGGTCAAAAGTGGATTATTTTAAAAACCAGAT   540

Qy    541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAGGACATAACAATAAC   600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAGGACATAACAATAAC   600

Qy    601 AGCAAATCAAAATCCGCAAATGCAAATTCCGCAGGAGAAATGGGGACTTTCATAAC   660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCAAATCAAAATCCGCAAATGCAAATTCCGCAGGAGAAATGGGGACTTTCATAAC   660
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Qy   4501 ATTTTGATATTTGATAATCATATTCATTATCATTTGTTCCTTTGTAATCTATATTTT   4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 ATTTTGATATTTGATAATCATATTCATTATCATTTGTTCCTTTGTAATCTATATTTT   4560

Qy   4561 ATATATTTGAAAACATCTTCTGAGAAGAGTTCCCCAGATTCCACCATGAGGTTCTTGG   4620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 ATATATTTGAAAACATCTTCTGAGAAGAGTTCCCCAGATTCCACCATGAGGTTCTTGG   4620

Qy   4621 CATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA   4680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 CATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA   4680

Qy   4681 TGCAAGACTGAAATTAGAAAGTTCTCCAAAGATACACAGTTGTTTTAAAGTTAGGGGTG   4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 TGCAAGACTGAAATTAGAAAGTTCTCCAAAGATACACAGTTGTTTTAAAGTTAGGGGTG   4740

Qy   4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTCGGTAGGGTGCTGTC   4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTCGGTAGGGTGCTGTC   4800

Qy   4801 CTTGTGTTCTGGCTGGCTGTTATTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT   4860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 CTTGTGTTCTGGCTGGCTGTTATTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT   4860

Qy   4861 GGATCTCCAGTTCCTAGCATAGTAGTTGCCTGGCACATAGTGCAGGTTCTCAATGAGTTGCAGAG   4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 GGATCTCCAGTTCCTAGCATAGTAGTTGCCTGGCACATAGTGCAGGTTCTCAATGAGTTGCAGAG   4920

Qy   4921 TGAATGGAAATATAAACTAGAAATAATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG   4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 TGAATGGAAATATAAACTAGAAATAATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG   4980

Qy   4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTAAACCAGGTGAGATA   5040
          ||||||||||||||||||||||||||||||||     ||||||||||||||||
Db   4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTAAACCAGGTGAGATA   5040

Qy   5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC   5100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC   5100

Qy   5101 CAAACAGACTTCTGGAAGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC   5160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 CAAACAGACTTCTGGAAGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC   5160

Qy   5161 CCTGTGCACAGCCCCACCCACCTCACGTGGCCACCTCGTCTTCCCCCATGAAGGGCTG   5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 CCTGTGCACAGCCCCACCCACCTCACGTGGCCACCTCGTCTTCCCCCATGAAGGGCTG   5220

Qy   5221 GCTCCCAGTATATATAAACCTCTCTGGAGCTCGGGAGCTCGGGCATGAGCCAGCAAGG   5271
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 GCTCCCAGTATATATAAACCTCTCTGGAGCTCGGGAGCTCGGGCATGAGCCAGCAAGG   5271
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RESULT 6
US-08-938-669-1
; Sequence 1, Application US/0938669
; GENERAL INFORMATION:
; APPLICANT:  Nguyen, Thai D.
; APPLICANT:  Polansky, Jon R.
; TITLE OF INVENTION:  METHODS FOR THE DIAGNOSIS,
; TITLE OF INVENTION:  PROGNOSIS AND TREATMENT OF GLAUCOMA AND RELATED DISEASE
; TITLE OF INVENTION:  S
; NUMBER OF SEQUENCES:  32
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Howrey & Simon
;   STREET:  1299 Pennsylvania Avenue, N.W.
;   CITY:  Washington
;   STATE:  DC
;   COUNTRY:  USA
;   ZIP:  20004-2402
; COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Diskette
;   COMPUTER:  IBM Compatible
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Thu Jan 26 14:20:40 2006   us-09-227-881-34.rnpm

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Qy    661  AGTGATTAGGCAGTTGACCATGTTCGGCAACACCTCCCGTCTCATACCAGGGAACACAAAA  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  AGTGATTAGGCAGTTGACCATGTTCGGCAACACCTCCCGTCTCATACCAGGGAACACAAAA  720

Qy    721  ATTGACTAGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAA   780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  ATTGACTAGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAA   780

Qy    781  GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA   840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA   840

Qy    841  GGGACCCTGAGGCATTTGCCCTTTAGGAAGGCCAGTTTCTTAAGGAATCTTAAGAAACTC   900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  GGGACCCTGAGGCATTTGCCCTTTAGGAAGGCCAGTTTCTTAAGGAATCTTAAGAAACTC   900

Qy    901  TTGAAAGATCATGAATTTAACCATTTAAGTATAAAACAAATAAATATGGCATGCATAATCAG  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  TTGAAAGATCATGAATTTAACCATTTAAGTATAAAACAAATAAATATGGCATGCATAATCAG  960

Qy    961  TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020

Qy   1021  GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTCAGAATGATC  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTCAGAATGATC  1080

Qy   1081  TGTCATAGCCCTCACACAACAGGCCCGATGGTGTCTGACTACAACCACATCTACAACCCAA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  TGTCATAGCCCTCACACAACAGGCCCGATGGTGTCTGACTACAACCACATCTACAACCCAA  1140

Qy   1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC  1200

Qy   1201  TGTGCAGCCGACTACACCGGCTCCCAGAGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  TGTGCAGCCGACTACACCGGCTCCCAGAGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT  1260

Qy   1261  TACAGCCAGAGAGTCTTGTGAGGTGAGGGTGAGGTGTCTTGTTACACCTGTATGTCTCTAC  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  TACAGCCAGAGAGTCTTGTGAGGTGAGGGTGAGGTGTCTTGTTACACCTGTATGTCTCTAC  1320

Qy   1321  ACCTGAGCTCACTGCACAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  ACCTGAGCTCACTGCACAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC  1380

Qy   1381  CGCGTAGCTGGGACTACAGGCGCACGGCGCACGCCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG  1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CGCGTAGCTGGGACTACAGGCGCACGGCGCACGCCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG  1440

Qy   1441  GTTTCACCATATTAGCCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC  1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  GTTTCACCATATTAGCCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC  1500

Qy   1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGGCCCCGGCCAAGGGTCAGTGT  1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGGCCCCGGCCAAGGGTCAGTGT  1560

Qy   1561  TTAATAAGGAATAACTTGAATGGTTACTAAACCAACAGGGAAAACAGACAAAGCTGTGA  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  TTAATAAGGAATAACTTGAATGGTTACTAAACCAACAGGGAAAACAGACAAAGCTGTGA  1620

Qy   1621  TAATTTCAGGGATTCTTGGGATGGGGATGGGGAATGGTGCCATGGGCCTAGCCCTAGTCCCAGAC  1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  TAATTTCAGGGATTCTTGGGATGGGGATGGGGAATGGTGCCATGGGCCTAGCCCTAGTCCCAGAC  1680

Qy   1681  CACTGGTCCTCATCACTTTCTTCCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  CACTGGTCCTCATCACTTTCTTCCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT  1740

Qy   1741  CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG  1800
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Db   1741  CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG  1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1801  TTCCATTTGGGGCCATCTGTGTGTGTATAGGGGAGGGGCATACCCAGAGACTCCT  1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  TTCCATTTGGGGCCATCTGTGTGTGTATAGGGGAGGGGCATACCCAGAGACTCCT  1860

Qy   1861  TGAAGCCCCGGCAGAGGTTCCTCTCCAGTCGTGGGGGAGCCCCTGGGGGGTCC  1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  TGAAGCCCCGGCAGAGGTTCCTCTCCAGTCGTGGGGGAGCCCCTGGGGGGTCC  1920

Qy   1921  TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTGTTATCACTCTCTAGG  1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTGTTATCACTCTCTAGG  1980

Qy   1981  GACCTGTTGCTTTCTATTTCTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT  2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  GACCTGTTGCTTTCTATTTCTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT  2040

Qy   2041  TATTGAGTACTTATATCTGCCAGACACCAGACAAAATGGTGAGCAAAGCAGTCACTGC  2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  TATTGAGTACTTATATCTGCCAGACACCAGACAAAATGGTGAGCAAAGCAGTCACTGC  2100

Qy   2101  CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAATTAATAGCCA  2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAATTAATAGCCA  2160

Qy   2161  GCCAACTTAAACCCAGTGCTGAAAGAAATGAAATAAACCATCTTGAAGAATTCGTGCGC  2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  GCCAACTTAAACCCAGTGCTGAAAGAAATGAAATAAACCATCTTGAAGAATTGTGCGC  2220

Qy   2221  AGCATCCCTAACAAGGCCACCTCCTAGCGCCCCTGCTCCCATCGTGCCCCGGAGG  2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  AGCATCCCTAACAAGGCCACCTCCTAGCGCCCCTGCTCCCATCGTGCCCCGGAGG  2280

Qy   2281  CCCCCAAGCCGAGTCTTCCAAGCCTCCTCCTCATCAGTCAGCGCTGCAGCTGGCCT  2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  CCCCCAAGCCGAGTCTTCCAAGCCTCCTCCTCATCAGTCAGCGCTGCAGCTGGCCT  2340

Qy   2341  GCCTCGCTTCCCGTGAATCGTCCGGTGCATCGAGCTGGAGACTCTGGCTCTCCAGGCT  2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  GCCTCGCTTCCCGTGAATCGTCCGGTGCATCGAGCTGGAGACTCTGGCTCTCCAGGCT  2400

Qy   2401  CCAGAAAGGAAATGGAGAGGAAACTAGTCTAACGGAAATCTGGAGGGATGGGGACTGCAGGGAG  2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  CCAGAAAGGAAATGGAGAGGAAACTAGTCTAACGGAAATCTGGAGGGATGGGGACTGCAGGGAG  2460

Qy   2461  CTCAGAGGGAAAAGGGGCCTCCAGGTCCAGGAATTCCAGGAAGGCTCAGGGAG  2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  CTCAGAGGGAAAAGGGGCCTCCAGGTCCAGGAATTCCAGGAAGGCTCAGGGAG  2520

Qy   2521  TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAAGGCAAGCTGAA  2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAAGGCAAGCTGAA  2580

Qy   2581  GCTGCCCAGAGTGTTCAGTTGTGTTCACGGGGCTCGGGAGTTTTCCGTTGCTTCCTGTGAGC  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  GCTGCCCAGAGTGTTCAGTTGTGTTCACGGGGCTCGGGAGTTTTCCGTTGCTTCCTGTGAGC  2640

Qy   2641  CTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC  2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  CTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC  2700

Qy   2701  ATAAAGTCAGCTGTTAAAATTCCAGGGTGCATGGGTTTCTTCACGGGCCTTTAT  2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  ATAAAGTCAGCTGTTAAAATTCCAGGGTGCATGGGTTTCTTCACGGGCCTTTAT  2760

Qy   2761  TTAATGGGAATATAGGAAGCGAGCTCATTTCGTAATTCACGGAAGAGTGAC  2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  TTAATGGGAATATAGGAAGCGAGCTCATTTCGTAATTCACGGAAGAGTGAC  2820

Qy   2821  TGGAGTCTTTTCTTTCATCGTCTCTGGGCAACTACTCAGCCCTGTGGTCTTGGCTTA  2880
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Qy  3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTCTCCACATGTGTTCTCGGAGGTGAGTCTGCCAGGG 4019
         ||||||||||||||||||||||||||||||||||     ||| |||||||||||||||||||||
Db  3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTCTTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019

Qy  4020 CAGTTTGAAAATTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4020 CAGTTTGAAAATTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079

Qy  4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTAAAGTTACTTCTGACACAGTTTTGGTATA 4139
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTAAAGTTACTTCTGACACAGTTTTGGTATA 4139

Qy  4140 TTTATTGGCTATTGCCATTGCTTTTTGTTTTTCTCTTGGGTTAATAATGTAAAGCA 4199
         ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db  4140 TTTATTGGCTATTGCCATTGCTTTTTGTTTTTCTCTTGGGTTATTAATGTAAAGCA 4199

Qy  4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTGAATGAGAAAAATTACATTT 4259
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTGAATGAGAAAAATTACATTT 4259

Qy  4260 TTGTTTTTACCACCTTCTAACTAAATTAACATTTATTCCATTGCGAATAGAGCCATAA 4319
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4260 TTGTTTTTACCACCTTCTAACTAAATTAACATTTATTCCATTGCGAATAGAGCCATAA 4319

Qy  4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379

Qy  4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439

Qy  4440 ACTTTGAAATTAGACCTCCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4440 ACTTTGAAATTAGACCTCCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499

Qy  4500 AATTTTGATATTTTGATAATCATTTGTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4500 AATTTTGATATTTTGATAATCATTTGTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559

Qy  4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTCACCAATGAGGTTCTTG 4619
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTCACCAATGAGGTTCTTG 4619

Qy  4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTCCTGAG 4679
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTCCTGAG 4679

Qy  4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGGT 4739
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGGT 4739

Qy  4740 GAGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4740 GAGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799

Qy  4800 CCTTGTGTTCTGGCTGGCTGTATTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4800 CCTTGTGTTCTGGCTGGCTGTATTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859

Qy  4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTTGCAGGTTCTCAATGAGTTTGCAGA 4919
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTTGCAGGTTCTCAATGAGTTTGCAGA 4919

Qy  4920 GTGAATGGAAATATAAACTAGAAATATCCTTGTTGAAATCAGCACCAGTAGTCCTG 4979
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4920 GTGAATGGAAATATAAACTAGAAATATCCTTGTTGAAATCAGCACCAGTAGTCCTG 4979

Qy  4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTAAAACCAGGTGAGAT 5039
         |||||||||||||||||||||||||||||||||||||||||||||
Db  4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
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Db  2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880

Qy  2881 TGCCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTCTTTCTTGGTTCTGCCATT 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 TGCCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTCTTTCTTGGTTCTGCCATT 2940

Qy  2941 GGTTGGCTGTGCGACCGGTGGGCAAGTGTCTCTCCTTCCTTCCCTGGGCCATAGTCTTCTCTCGCT 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 GGTTGGCTGTGCGACCGGTGGGCAAGTGTCTCTCCTTCCTTCCCTGGGCCATAGTCTTCTCTCGCT 3000

Qy  3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTTGTGAACACTTCCCTGATTCTCTGTGAGGGG 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTTGTGAACACTTCCCTGATTCTCTGTGAGGGG 3060

Qy  3061 GGATGTTGAGAGGGAAGGAGGAGGAGGCAGAGCTGGAGCAGGCCACAGGGAGGTGGAGGG 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 GGATGTTGAGAGGGAAGGAGGAGGAGGCAGAGCTGGAGCAGGCCACAGGGAGGTGGAGGG 3120

Qy  3121 GGACAGGAAGGCAGGCAGAGAAGCTGGGTGCTCCATCAGTCCTCCACTCAGTCCTCAGACTC 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 GGACAGGAAGGCAGGCAGAGAAGCTGGGTGCTCCATCAGTCCTCCACTCAGTCCTCAGACTC 3180

Qy  3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCCACATTTTCCT 3240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCCACATTTTCCT 3240

Qy  3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAATAACCAAAAGAATGCAGAGACTAACTGGT 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAATAACCAAAAGAATGCAGAGACTAACTGGT 3300

Qy  3301 GGTAGCTTTGCCTGGCATTCAAAAACTGGGCCAGGCAAGTGGAAAATGCCAGAGATTG 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 GGTAGCTTTGCCTGGCATTCAAAAACTGGGCCAGGCAAGTGGAAAATGCCAGAGATTG 3360

Qy  3361 TTAAAACTTTCACCCTGACCAGCACCCCACGCACCCACGCTCAGCAGCACGG 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 TTAAAACTTTCACCCTGACCAGCACCCCACGCACCCACGCTCAGCAGCACGG 3420

Qy  3421 AGTGACCTGCAGCGCGCAGGGGAGGAGAGAAAGAGGGATAGTGTATGAGCAAGAAAG 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 AGTGACCTGCAGCGCGCAGGGGAGGAGAGAAAGAGGGATAGTGTATGAGCAAGAAAG 3480

Qy  3481 ACAGATTCATTCAAGGGCAGTGGAATTGACCACCAGTAGTCCCGTGATCCTGG 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 ACAGATTCATTCAAGGGCAGTGGAATTGACCACCAGTAGTCCCGTGATCCTGG 3540

Qy  3541 GTTCTCAGGAGGCAGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGTCGGGGAGA 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 GTTCTCAGGAGGCAGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGTCGGGGAGA 3600

Qy  3601 CCTGATTTCTAATACTATATTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 CCTGATTTCTAATACTATATTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660

Qy  3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTGT 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTGT 3720

Qy  3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTCTTTTAACAGGAAGAAAAACATTCCTAAGAG 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTCTTTTAACAGGAAGAAAAACATTCCTAAGAG 3780

Qy  3781 TAAAGCCAAACAGATTCAAGCCTAGTCTTGCTGACTATATGATTGGTTTTTGAAAAAT 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 TAAAGCCAAACAGATTCAAGCCTAGTCTTGCTGACTATATGATTGGTTTTTGAAAAAT 3840

Qy  3841 CATTTCAGCGATGTTTACTATCTGATTCAGAGAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 CATTTCAGCGATGTTTACTATCTGATTCAGAGAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

Qy  3901 TAAACAAACACCCAGTTGTAAATGTCCAAGTTCAGGCTTAACTGCGAGAACCAATCAAA- 3959
         ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db  3901 TAAACAAACACCCATTGTAAATGTCCAAGTTCAGGCTTAACTGCGAGAACCAATCAAAT 3960
```

Qy   5040 ATAGAGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAGAAACT 5099
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5040 ATAGAGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAGAAACT 5099

Qy   5100 CCAAACAGACTTCTGGAAGGTTATTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5100 CCAAACAGACTTCTGGAAGGTTATTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159

Qy   5160 CCCTGTGCACAGCCCACCCAGCCTCACGTGCCACCTCGTCTTCCCCCATGAAGGGCT 5219
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5160 CCCTGTGCACAGCCCACCCAGCCTCACGTGCCACCTCGTCTTCCCCCATGAAGGGCT 5219

Qy   5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCCAAGG 5271
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCCAAGG 5271

RESULT 7
US-09-227-881-1
; Sequence 1, Application US/09227881
; GENERAL INFORMATION:
;   APPLICANT: Nguyen, Thai D.
;   APPLICANT: Polansky, Jon R.
;   APPLICANT: Chen, Pu
;   APPLICANT: Chen, Hua
;   TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
;   CURRENT APPLICATION NUMBER: US/09/227,881
;   CURRENT FILING DATE: 1999-01-11
;   EARLIER APPLICATION NUMBER: US 08/938,669
;   EARLIER FILING DATE: 1997-09-26
;   NUMBER OF SEQ ID NOS: 36
;   SOFTWARE: Microsoft Word 97
; SEQ ID NO 1
;   LENGTH: 5300
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-227-881-1

  Query Match   99.5%;   Score 5246.4;   DB 22;   Length 5300;
  Best Local Similarity 99.9%;   Pred. No. 0;
  Matches 5269;   Conservative 0;   Mismatches 0;   Indels 2;   Gaps 2;

Qy   1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG   60

Qy   61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAAATCA 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAAATCA 120

Qy   121 GGAAGAAGGAGTATCCACGTAGCCAAGTGTCCAGGCGTGTCCAGGCGTGTCTTATTTTAGTGA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAAGAAGGAGTATCCACGTAGCCAAGTGTCCAGGCGTGTCCAGGCGTGTCTTATTTTAGTGA 180

Qy   181 CAGATGTGCTCCTGACAGAGCTATTCTTCAGGAAACATCACCCAATAATGGTAAATC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CAGATGTGCTCCTGACAGAGCTATTCTTCAGGAAACATCACCCAATAATGGTAAATC 240

Qy   241 CATCAAACAGAGCTAAGAAACAGGAATGAGATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CATCAAACAGAGCTAAGAAACAGGAATGAGATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy   301 GAGAGCAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAAGAGTGTTCCAAATTGG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GAGAGCAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAAGAGTGTTCCAAATTGG 360

Qy   361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAAGAGTGTTTCCAAATTGG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAAGAGTGTTTCCAAATTGG 420

Qy   421 TAATTAAGTAATTGTTCCTTGGGAAGAGACCTTCCATGTGAGCTTGATGGGAAAATGGGAA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TAATTAAGTAATTGTTCCTTGGGAAGAGACCTTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy   481 AAACGTCAAAAGCATGATCTGATCAGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AAACGTCAAAAGCATGATCTGATCAGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy   541 GGCATCACTCTGGGAGGCAAGTTCAGGAGGTCATGTTAGCAAGGACTAACAATAAC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGCATCACTCTGGGAGGCAAGTTCAGGAGGTCATGTTAGCAAGGACTAACAATAAC 600

Qy   601 AGCAAAATCAAAATTCCGAAATGCAGGAGGACTGGGAAAGCTTTCATAAC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AGCAAAATCAAAATTCCGAAATGCAGGAGGACTGGGAAAGCTTTCATAAC 660

Qy   661 AGTGATTAGGCAGTTGACCATGTTGCCAACACCTCCCGTCTATACCAGGGAACACAAAA 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGTGATTAGGCAGTTGACCATGTTGCCAACACCTCCCGTCTATACCAGGGAACACAAAA 720

Qy   721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGAAATGGAAAACTGAGAAAACTGAGAGAGCAAAACAAAA 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGAAATGGAAAACTGAGAAAACTGAGAGAGCAAAACAAAA 780

Qy   781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy   841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy   901 TTGAAAGATCATGAATTTAACCATTTAAGTATAAAAACAAATATGCGATGCATAATCAG 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TTGAAAGATCATGAATTTAACCATTTAAGTATAAAAACAAATATGCGATGCATAATCAG 960

Qy   961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAGGATAACGTGTCCCAGCTCC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAGGATAACGTGTCCCAGCTCC 1020

Qy   1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTCAGAATGATC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTCAGAATGATC 1080

Qy   1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACACACCATCTACAACCCAA 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACACACCATCTACAACCCAA 1140

Qy   1141 GTGCCTCAACCATTGTTAACGTCATCTCAGTAGTCCATTACAAATGCCACCTCCCC 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GTGCCTCAACCATTGTTAACGTCATCTCAGTAGTCCATTACAAATGCCACCTCCCC 1200

Qy   1201 TGTGCAGCCCATCCCGCTCCACAGGAGTCTCCCACTCTAGACTTCTGCATCACGATGT 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TGTGCAGCCCATCCCGCTCCACAGGAGTCTCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy   1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTCACCTACCTGTATGCTCTAC 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTCACCTACCTGTATGCTCTAC 1320

Qy   1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCGTGTCTCAGCCTCC 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCGTGTCTCAGCCTCC 1380

Qy   1381 CGCGTAGCTGGGACTACAGGCGCCACCCGGCTCGGTCTTAGTGATTAGGTTAGTAGAGATGG 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CGCGTAGCTGGGACTACAGGCGCCACCCGGCTCGGTCTTAGTGATTAGGTTAGTAGAGATGG 1440

Qy   1441 GTTTCACCATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GTTTCACCATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy   1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGGAGCCATGAGTCACCGGCCCGCCAAGGGTCAGTGT 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGGAGCCATGAGTCACCGGCCCGCCAAGGGTCAGTGT 1560

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Qy   1561  TTAATAAGGAATAATAACTTGAATGGTTTACTAAACCAACAGGAGGAAACAGAGACAAAAGCTGTGA  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  TTAATAAGGAATAATAACTTGAATGGTTTACTAAACCAACAGGAGGAAACAGAGACAAAAGCTGTGA  1620

Qy   1621  TAATTTCAGGGATTCTTGGGATGGGAATGGTGCCATGAGCTGCCTAGTGTGCCAGAC  1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  TAATTTCAGGGATTCTTGGGATGGGAATGGTGCCATGAGCTGCCTAGTGTGCCAGAC  1680

Qy   1681  CACTGGTCCTCATCACTTCTTCCCTCAATCCTCATTTCAGGCTAAGTTACCATTTTATT  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  CACTGGTCCTCATCACTTCTTCCCTCAATCCTCATTTCAGGCTAAGTTACCATTTTATT  1740

Qy   1741  CACCATGCTTTGTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG  1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  CACCATGCTTTGTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG  1800

Qy   1801  TTCCATTTGGGGCCATCTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT  1860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  TTCCATTTGGGGCCATCTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT  1860

Qy   1861  TGAAGCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC  1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  TGAAGCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC  1920

Qy   1921  TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTGTTTGTTATCACTTCTAGG  1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTGTTTGTTATCACTTCTAGG  1980

Qy   1981  GACCTGTTGCTTTCTATTTCGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT  2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  GACCTGTTGCTTTCTATTTCGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT  2040

Qy   2041  TATTTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC  2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  TATTTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC  2100

Qy   2101  CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAGAGAAAAATTAATAGCCA  2160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAGAGAAAAATTAATAGCCA  2160

Qy   2161  GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC  2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC  2220

Qy   2221  AGCATCCCTAACAAGGCCACCTCCCTAGCGCCCCTGCCTCCATCGTCGCCCGGAGG  2280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  AGCATCCCTAACAAGGCCACCTCCCTAGCGCCCCTGCCTCCATCGTCGCCCGGAGG  2280

Qy   2281  CCCCCAAGCCCGAGTCTTCCACGTCTCCACGTCCCAGCCTCACAGCTCACAGCCTGGCCT  2340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  CCCCCAAGCCCGAGTCTTCCACGTCTCCACGTCCCAGCCTCACAGCTCACAGCCTGGCCT  2340

Qy   2341  GCCTCGCTTCCCGTGAATCGTCCTGTCATCGTGAGCTGGAGACTCCTTGGCTGTCCAGCT  2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  GCCTCGCTTCCCGTGAATCGTCCTGTCATCGTGAGCTGGAGACTCCTTGGCTGTCCAGCT  2400

Qy   2401  CCGAAAGGAAATGGAGGGGAAACTGGAGGGGAAATCTGGAGGGGAACAGTGTTTC  2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  CCGAAAGGAAATGGAGGGGAAACTGGAGGGGAAATCTGGAGGGGAACAGTGTTTC  2460

Qy   2461  CTTCAGGAGGGGAAAAGGCCTCCCACGTCCACGTCCCACCTCCAGGAGGTGGGGACTGCAGGGAG  2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  CTTCAGGAGGGGAAAAGGCCTCCCACGTCCACGTCCCACCTCCAGGAGGTGGGGACTGCAGGGAG  2520

Qy   2521  TGGGGACGCTGGGGCTGAGCGGGCTGCTGAGGGTGAAAAGGGCAAGGCTGAA  2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  TGGGGACGCTGGGGCTGAGCGGGCTGCTGAGGGTGAAAAGGGCAAGGCTGAA  2580

Qy   2581  GCTGCCCAGATGTTCAGTGTTGTTCAGTGTTGTTCCGTTCCGTTGCTTCCGTGTGAGC  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  GCTGCCCAGATGTTCAGTGTTGTTCAGTGTTGTTCCGTTCCGTTGCTTCCGTGTGAGC  2640

Qy   2641  CTTTTTATCTTTCTCTGCTTGGAGGAGAAGAGTCTATTTCATGAGAGGGGATGTGCAGTTTC  2700
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  CTTTTTATCTTTCTCTGCTTGGAGGAGAAGAGTCTATTTCATGAGAGGGGATGTGCAGTTTC  2700

Qy   2701  ATAAAGTCAGCTGTTAAAATTCCAGGTGTTTCCTTCACGGAAGGCCTTTAT  2760
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  ATAAAGTCAGCTGTTAAAATTCCAGGTGTTTCCTTCACGGAAGGCCTTTAT  2760

Qy   2761  TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTAATTCACGGAAGAAGTGAC  2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTAATTCACGGAAGAAGTGAC  2820

Qy   2821  TGGAGTCTTTTCTTTCATGTCTTCTCGGGCAACTACTCAGCCCTGTGTGGACTTGGCTTA  2880
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  TGGAGTCTTTTCTTTCATGTCTTCTCGGGCAACTACTCAGCCCTGTGTGGACTTGGCTTA  2880

Qy   2881  TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTCTTTCTGGTTCTCGCCATT  2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTCTTTCTGGTTCTCGCCATT  2940

Qy   2941  GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCCTCCCTGCCAAGCACCCGGGGTCC  3000
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCCTCCCTGCCAAGCACCCGGGGTCC  3000

Qy   3001  ATAAAGACCCTTGCAGCTCCAGCTTCGTGTTCTGTGAACACTTCCCTGATTCTTCGTGAGGGGG  3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  ATAAAGACCCTTGCAGCTCCAGCTTCGTGTTCTGTGAACACTTCCCTGATTCTTCGTGAGGGGG  3060

Qy   3061  GGATGTTGAGAGGAGGCAGAGCTGAGCCACAGGGGAGGG  3120
           ||||||||||||||||||||||||||||||||||||||||
Db   3061  GGATGTTGAGAGGAGGCAGAGCTGAGCCACAGGGGAGGG  3120

Qy   3121  GGACAGGAGGCAGGCAGGCAGAGCTGGGTGCTTCCATCGTCCTCACTGATCACGTCAGACTC  3180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121  GGACAGGAGGCAGGCAGGCAGAGCTGGGTGCTTCCATCGTCCTCACTGATCACGTCAGACTC  3180

Qy   3181  CAGGACCCAGAGCCACCACAATGCTTCAGGAAAGCTCAATGAACCAACAGCCACATTTTCCT  3240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181  CAGGACCCAGAGCCACCACAATGCTTCAGGAAAGCTCAATGAACCAACAGCCACATTTTCCT  3240

Qy   3241  TCCCTAAGCAGCATAGACAATGGCATTTGCCAATAACCAACAAAAAGAATGCAGAGACTAACTGGT  3300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241  TCCCTAAGCAGCATAGACAATGGCATTTGCCAATAACCAACAAAAAGAATGCAGAGACTAACTGT  3300

Qy   3301  GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCCACGCAGTGACTGCTGACAGAGATTG  3360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301  GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCCACGCAGTGACTGCTGACAGAGATTG  3360

Qy   3361  TTAAACTTTTCACCCTGACCAGCCAGCAGTGTGGGGGAAAAATCAGTTCAAGGGAAGCACGG  3420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361  TTAAACTTTTCACCCTGACCAGCCAGCAGTGTGGGGGAAAAATCAGTTCAAGGGAAGCACGG  3420

Qy   3421  AGTGACCTGCAGCGCAGGGGAGGAAGGGATAGTGTATGAGCAAGAAAG  3480
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421  AGTGACCTGCAGCGCAGGGGAGGAAGGGATAGTGTATGAGCAAGAAAG  3480

Qy   3481  ACAGATCATTCAAGGGACGGCAGTGGGAATTGACCACAGGGGATTATAGTCCACGTGATCCTG  3540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481  ACAGATCATTCAAGGGACGGCAGTGGGAATTGACCACAGGGGATTATAGTCCACGTGATCCTG  3540

Qy   3541  GTTCTAGGAGGGCAGGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGGGAGA  3600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541  GTTCTAGGAGGGCAGGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGGGAGA  3600

Qy   3601  CCTGATTTCTAATACTATATTTCCTTTACAAGCTGAGTAATTCTGAGCAAG  3660
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601  CCTGATTTCTAATACTATATTTCCTTTACAAGCTGAGTAATTCTGAGCAAG  3660

Qy   3661  GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT  3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661  GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT  3720

Qy   3721  GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTAACAGGAAGAAAACATTCCTAAGAG  3780
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Qy  4860  TGGATCTCCAGTTCCTAGCATAGTAGTGTGGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA  4919
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4860  TGGATCTCCAGTTCCTAGCATAGTAGTGTGGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA  4919

Qy  4920  GTGAATGGAAATATAAACTAGAAATATATCCTGTGTGAAATCAGCACCAGTAGTCCTG  4979
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4920  GTGAATGGAAATATAAACTAGAAATATATCCTGTGTGAAATCAGCACCAGTAGTCCTG  4979

Qy  4980  GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTAAAACCAGGTGAGGAT  5039
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  4980  GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTAAAACCAGGTGAGGAT  5039

Qy  5040  ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTAAAAGAAACT  5099
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5040  ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTAAAAGAAACT  5099

Qy  5100  CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTCGCAGCGTGAAGGCAACCC  5159
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5100  CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTCGCAGCGTGAAGGCAACCC  5159

Qy  5160  CCCTGTGCACAGCCCACCAGCCTCACGTGCCCACCTCGTCTTCCCCATGAAGGGCT  5219
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5160  CCCTGTGCACAGCCCACCAGCCTCACGTGCCCACCTCGTCTTCCCCATGAAGGGCT  5219

Qy  5220  GGCTCCCCAGTATATATAAAACCTCTCGGAGCTCGGGCATGAGCCAGCAAGG  5271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5220  GGCTCCCCAGTATATATAAAACCTCTCGGAGCTCGGGCATGAGCCAGCAAGG  5271
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RESULT 8
US-09-985-637A-1
; Sequence 1, Application US/0998563 7A
; GENERAL INFORMATION:
; APPLICANT: Polansky, Jon
; TITLE OF INVENTION: METHODS TO SCREEN AND TREAT INDIVIDUALS WITH GLAUCOMA OR THE PF
; TITLE OF INVENTION: TO DEVELOP GLAUCOMA
; FILE REFERENCE: 13587.296
; CURRENT APPLICATION NUMBER: US/09/985,637A
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-985-637A-1

Query Match   99.5%; Score 5246.4; DB 38; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5269; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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Qy     1  ATCTTTGTTCAGTTTACCTTACCTTCAGGGCTATTATGATGGGCTATTATGATGAAATGAAAG    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ATCTTTGTTCAGTTTACCTTACCTTCAGGGCTATTATGATGGGCTATTATGATGAAATGAAAG    60

Qy    61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTGGCAGGATGATAAAAGAATCA   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTGGCAGGATGATAAAAGAATCA   120

Qy   121  GGAAGAGGAGTATCCACGTTAGCCAAGTGTCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA   180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GGAAGAGGAGTATCCACGTTAGCCAAGTGTCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA   180

Qy   181  CAGATGTTGCTCCTGACAGAAGAAGCTATTCTTCAGGAAAACATCACATCCAATATGTAAATC   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  CAGATGTTGCTCCTGACAGAAGAAGCTATTCTTCAGGAAAACATCACATCCAATATGTAAATC   240

Qy   241  CATCAAACAGAGACTAAGAAACAGGAATGAGATGAGATTGCCCAAGGAAAATGCCAG   300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  CATCAAACAGAGACTAAGAAACAGGAATGAGATGAGATTGCCCAAGGAAAATGCCAG   300

Qy   301  GAGAGCAAATAATGATGAAAATAACTTTTCCCTTTGTTTTTAATTCAGGAAAAATG   360
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Db  3721  GGAGTTAGCAGCACAAGGGCAATCCCGTTCTTTCTTTAACAGGAAGAAACATTCCTAAGAG  3780

Qy  3781  TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGCTAGTATGATATGATTGGTTTTTTGAAAAAT  3840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781  TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGCTAGTATGATATGATTGGTTTTTTGAAAAAT  3840

Qy  3841  CATTTCAGCGATGTTACTATCTGATTCAGAAAAATGAGACTAGTACCCTTTGGTCAGCTG  3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841  CATTTCAGCGATGTTACTATCTGATTCAGAAAAATGAGACTAGTACCCTTTGGTCAGCTG  3900

Qy  3901  TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA-  3959
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Db  3901  TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT  3960

Qy  3960  AAGAATAGAATCTTTAGAGCAAACTGTGTTCTCCACATCTGGAGGTGAGTCTGCCAGGG  4019
          ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db  3961  AAGAATAGAATCTTTAGAGCAAACTGTGTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG  4019

Qy  4020  CAGTTTGGAAATATTACTTCACAAGTATTGACACTGTGTTGGTATTAACAACATAAAG  4079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4020  CAGTTTGGAAATATTACTTCACAAGTATTGACACTGTGTTGGTATTAACAACATAAAG  4079

Qy  4080  TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTGGTATA  4139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4080  TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTGGTATA  4139

Qy  4140  TTTATTGGCTATTGCCATTTGCTTTTGTTTTTCTCTTTGGGTTTATTAATGTAAAGCA  4199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4140  TTTATTGGCTATTGCCATTTGCTTTTGTTTTTCTCTTTGGGTTTATTAATGTAAAGCA  4199

Qy  4200  GGGATTATTAACCTACAGTCCAGAAAGCCTGGAATTGAATGAGAGAAAAATTACATTT  4259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4200  GGGATTATTAACCTACAGTCCAGAAAGCCTGGAATTGAATGAGAGAAAAATTACATTT  4259

Qy  4260  TTGTTTTTACCACCTTCTAACTAAATTTAACATTTATTCCATTGCGAATAGAGCCATAA  4319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4260  TTGTTTTTACCACCTTCTAACTAAATTTAACATTTATTCCATTGCGAATAGAGCCATAA  4319

Qy  4320  ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT  4379
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4320  ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT  4379

Qy  4380  TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT  4439
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4380  TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT  4439

Qy  4440  ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTGTTTTAACATATTAATAATAAACATGTTTAA  4499
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4440  ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTGTTTTAACATATTAATAATAAACATGTTTAA  4499

Qy  4500  AATTTGATATTTTGATATTTGATATTTGATATCATATTGTTTCCTTTGTAATCTATATTT  4559
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4500  AATTTGATATTTTGATATTTGATATTTGATATCATATTGTTTCCTTTGTAATCTATATTT  4559

Qy  4560  TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCCAATGAGGGTTCTTG  4619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4560  TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCCAATGAGGGTTCTTG  4619

Qy  4620  GCATGCACACACAGAGTAAGAAGTAAGAAGTAACATTGACATTGGTGGTGCCTGAG  4679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4620  GCATGCACACACAGAGTAAGAAGTAAGAAGTAACATTGACATTGGTGGTGCCTGAG  4679

Qy  4680  ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTGTTTTAAAGCTAGGGGT  4739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4680  ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTGTTTTAAAGCTAGGGGT  4739

Qy  4740  GAGGGGGGAAATCGCGCCTTCATAGGAATGCCTCCCCTGGAGCCTGGTGTCGTGT  4799
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4740  GAGGGGGGAAATCGCGCCTTCATAGGAATGCCTCCCCTGGAGCCTGGTGTCGTGT  4799

Qy  4800  CCTTGTGTTCTGGCTGTGTTATTTTTCTGTCCCGTACGTCTTACGGGTCTTAAAGGACTTGTT  4859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4800  CCTTGTGTTCTGGCTGTGTTATTTTTCTGTCCCGTACGTCTTACGGGTCTTAAAGGACTTGTT  4859
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Qy   1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTCAATTTTTGTATTGTTAGTAGAGATGGG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTCAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy   1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy   1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCCGCCCAAGGGTCAGTGT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCCGCCCAAGGGTCAGTGT 1560

Qy   1561 TTAATAAGGAATAACTTGAATGGTTACTAAACCAACAGGGAAACAACAGGGAAACAAAAGCTGTGA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TTAATAAGGAATAACTTGAATGGTTACTAAACCAACAGGGAAACAACAGGGAAACAAAAGCTGTGA 1620

Qy   1621 TAATTTCAGGGATTCTTGGGCATGGGGAATGGTGCCATGAGCTGCCTGCGCTGCCCAGTCCCAGAC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TAATTTCAGGGATTCTTGGGCATGGGGAATGGTGCCATGAGCTGCCTGCGCTGCCCAGTCCCAGAC 1680

Qy   1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy   1741 CACCACGTCTTTGTGGTAAGCCTCCACATCTGTGTGTATAGGGGAGGGGCATACCCCAGACTCCT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CACCACGTCTTTGTGGTAAGCCTCCACATCTGTGTGTATAGGGGAGGGGCATACCCCAGACTCCT 1800

Qy   1801 TTCCATTTGGGGCCATCTGTGTGTACTCGTTCATTCAGGCATTCATTGACAATT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 TTCCATTTGGGGCCATCTGTGTGTACTCGTTCATTCAGGCATTCATTGACAATT 1860

Qy   1861 TGAAGCCCCGGCGAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCCAAGCACCCGGGGTCC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TGAAGCCCCGGCGAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCCAAGCACCCGGGGTCC 1920

Qy   1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTGTTGTTTGTTTTCACTCTCTAGG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTGTTGTTTGTTTTCACTCTCTAGG 1980

Qy   1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCAGGCATTCATTCAGGCATTCATTGACAATT 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCAGGCATTCATTCAGGCATTCATTGACAATT 2040

Qy   2041 TATTGAGTACTTATATCTGCCACACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TATTGAGTACTTATATCTGCCACACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy   2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGAGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGAGAAGACGTGCAGAAGAAAATTAATAGCCA 2160

Qy   2161 GCCAACTTAAACCCAGTGCTGAAAGAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GCCAACTTAAACCCAGTGCTGAAAGAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy   2221 AGCATCCCTTAACAAGGCCACCTCCTAGCGCCCCTGCTGCCTCCATCGTGCCCGAGG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 AGCATCCCTTAACAAGGCCACCTCCTAGCGCCCCTGCTGCCTCCATCGTGCCCGAGG 2280

Qy   2281 CCCCCAAGCCCGAGTCTTCCAAGCTCTCCTCCATCAGTCAGCTGCCT 2340
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CCCCCAAGCCCGAGTCTTCCAAGCTCTCCTCCATCAGTCAGCTGCCT 2340

Qy   2341 GCCTCGCTTCCCGTGAATCGTCCTGGTCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 GCCTCGCTTCCCGTGAATCGTCCTGGTCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy   2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAAATCTGGAGGGGACAGTGTTTC 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAAATCTGGAGGGGACAGTGTTTC 2460

Qy   2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGACTGCAGGGAG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGACTGCAGGGAG 2520
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Db    301 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTGTTTTTAATTTCAGGAGAAAAAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy    361 ATGAGGACCAAAATCAATGAATAAGGAATAACAGCTCAGAAACAGCTCAGGAAAATGGAATGTTCCAAATTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAGGACCAAAATCAATGAATAAGGAATAACAGCTCAGAAACAGCTCAGGAAAATGGAATGTTCCAAATTGG 420

Qy    421 TAATTAAGTATTTGTTCCTTGGGAAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TAATTAAGTATTTGTTCCTTGGGAAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy    481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTTAAAAACCAGAT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTTAAAAACCAGAT 540

Qy    541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGACATAACAATAAC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGACATAACAATAAC 600

Qy    601 AGCAAAATCAAAATTCCGAAATGCAGGAGAAATGGGGACTTGGGAAAGCTTTCATAAC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCAAAATCAAAATTCCGAAATGCAGGAGAAATGGGGACTTGGGAAAGCTTTCATAAC 660

Qy    661 AGTGATTAGGCAGTTGACCATGTTCGCAACACTCCCGTCTCATACCAGGGAACACAAAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGTGATTAGGCAGTTGACCATGTTCGCAACACTCCCGTCTCATACCAGGGAACACAAAA 720

Qy    721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGGAAATATGAGAGCAAAACAAAA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGGAAATATGAGAGCAAAACAAAA 780

Qy    781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCACCAGTGCCCCTCAGCA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCACCAGTGCCCCTCAGCA 840

Qy    841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy    901 TTGAAAGATCATGAATTTTAACCATTTTAATAAAACAAATATGCATGACAATAATCAG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db.   901 TTGAAAGATCATGAATTTTAACCATTTTAATAAAACAAATATGCATGACAATAATCAG 960

Qy    961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATAACAAGGATAACGTGTCCAGGTCC 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATAACAAGGATAACGTGTCCAGGTCC 1020

Qy   1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCGTCTTTTCAGAATGATC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCGTCTTTTCAGAATGATC 1080

Qy   1081 TGTCATAGCCCTTCACACAGGCCCGATGTGTCTGACCATCTACAACCCAA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTCATAGCCCTTCACACAGGCCCGATGTGTCTGACCATCTACAACCCAA 1140

Qy   1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGGTCCCCATTACAAATGCCACCTCCCC 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGGTCCCCATTACAAATGCCACCTCCCC 1200

Qy   1201 TGTGCAGCCCATCCCGCTCCACACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TGTGCAGCCCATCCCGCTCCACACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy   1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTGAGGGTCTGTGTTCTTACACCTACCTGTATGCTCTAC 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTGAGGGTCTGTGTTCTTACACCTACCTGTATGCTCTAC 1320

Qy   1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCCAGGTTCAAGCAATTCTTCCTGTCTGTCAGCCTCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCCAGGTTCAAGCAATTCTTCCTGTCTGTCAGCCTCC 1380

Qy   1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTCAATTTTTGTATTGTTAGTAGAGATGGG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  3601 CCTGATTTCTAATACTATATTTTCCTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 CCTGATTTCTAATACTATATTTTCCTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660

Qy  3661 GTAGTAACTGAGGCGTGTAAGATTACTAGTTTCTCCTTATTAGGAGACTCTTTTCTCGT 3720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GTAGTAACTGAGGCGTGTAAGATTACTAGTTTCTCCTTATTAGGAGACTCTTTTCTCGT 3720

Qy  3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTCTTTTAACAGGAAGAAACATTCCTAAGAG 3780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTCTTTTAACAGGAAGAAACATTCCTAAGAG 3780

Qy  3781 TAAAGCCAAACAGATTCAAGCCTAGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 TAAAGCCAAACAGATTCAAGCCTAGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840

Qy  3841 CATTTCAGCGACGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTGGTCAGCTG 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 CATTTCAGCGACGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTGGTCAGCTG 3900

Qy  3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGACCAATCAAA- 3959
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901 TAAACAAACACCCATTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGACCAATCAAAT 3960

Qy  3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTCTCCACATCTGGAGGTGAGCTGCCAGGG 4019
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTCTCCAC-TCTGGAGGTGAGCTGCCAGGG 4019

Qy  4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGGTATTAACAACATAAAG 4079
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGGTATTAACAACATAAAG 4079

Qy  4080 TTGCTCAAAGGCAATCATTATTCAAGTATCATTATTCAAGTGGCTTAAAGTTACTCTGACAGTTTTGGTATA 4139
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4080 TTGCTCAAAGGCAATCATTATTCAAGTATCATTATTCAAGTGGCTTAAAGTTACTCTGACAGTTTTGGTATA 4139

Qy  4140 TTTATTGGCTATTGCCATTGCTTTTGTTTTTCTCTTTGGGTTTATTATGTAAAGCA 4199
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4140 TTTATTGGCTATTGCCATTGCTTTTGTTTTTCTCTTTGGGTTTATTATGTAAAGCA 4199

Qy  4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGAATTGAATGAGGAAAAATTACATT 4259
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGAATTGAATGAGGAAAAATTACATT 4259

Qy  4260 TTGTTTTTACCACCTTCTAACTAAATTAACATTTTATTCCATTGGAATAGAGCCATAA 4319
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4260 TTGTTTTTACCACCTTCTAACTAAATTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319

Qy  4320 ACTCAAAGTGGTAATAACAGTACCTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4320 ACTCAAAGTGGTAATAACAGTACCTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379

Qy  4380 TTTATACTATTACTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4380 TTTATATTACTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTTCAAAAACT 4439

Qy  4440 ACTTTGAAATTAGACCTTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4440 ACTTTGAAATTAGACCCCCTGCTGGATCTTGTTTTTAACATATTAATAATAAAACATGTTTAA 4499

Qy  4500 AATTTTGATATTTTGATAATCATATTGTTCCTTTGTAATCTATATATTT 4559
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  4500 AATTTTGATATTTTGATAATCATATTGTTCCTTTGTAATCTATATATTT 4559

Qy  4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCAGATTCACCAATGAGGTTCTTG 4619
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4560 TATATATTTGAAAAACATCTTTCTGAGAAGAGTTCCCAGATTCACCAATGAGGTTCTTG 4619

Qy  4620 GCATGCACACACACAGTGATTTAGAGAACTGATTTCAGTTCAAGGAGTCGGCCTGAG 4679
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4620 GCATGCACACACACAGTGATTTAGAGAACTGATTTCAGTTCAAGGAGTCGGCCTGAG 4679

Qy  4680 ATGCAAGAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
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Qy  2521 TGGGGACGCTGGGGCTGAGCGGCGGTGCTGCTGAAAAGGCAGGAGGCAAGGCTGAA 2580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 TGGGGACGCTGGGGCTGAGCGGCGGTGCTGCTGAAAAGGCAGGAGGCAAGGCTGAA 2580

Qy  2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTCGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640

Qy  2641 CTTTTATCTTTCTCCGCTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 CTTTTTATCTTTCTCCGCTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy  2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTCCTTCACGAAGGCCTTTAT 2760
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTCCTTCACGAAGGCCTTTAT 2760

Qy  2761 TTAATGGGAATATAGGAAGGCAGCTCATTTCCTAGCCGTTAATTCACGGAAGAAGTGAC 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 TTAATGGGAATATAGGAAGGCAGCTCATTTCCTAGCCGTTAATTCACGGAAGAAGTGAC 2820

Qy  2821 TGGAGTCTTTTCTTCTCATGTCTTCTGGGCAACTACTCAGCCCTGTGTGACTTGGCTTA 2880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 TGGAGTCTTTTCTTCTCATGTCTTCTGGGCAACTACTCAGCCCTGTGTGACTTGGCTTA 2880

Qy  2881 TGCAAGACGTCGAAAACCTTGGAATCAGGAGACTCGGTTTCTTCTGGTTTCTCGCCATT 2940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTCTTCTGGTTTCTCGCCATT 2940

Qy  2941 GGTTGGCTGTGTCGACCGTGGGCAAGTGTCTCTCCTCCCGGCCATAGTCTTCTCTCGCT 3000
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 GGTTGGCTGTGTCGACCGTGGGCAAGTGTCTCTCCTCCCGGCCATAGTCTTCTCTCGCT 3000

Qy  3001 ATAAAGACCCCTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 ATAAAGACCCCTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060

Qy  3061 GGGATGTTGAGGAGGAAGGACAGCAGCTCGAGCAGCAGCAGGAGGTGGAGGG 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 GGGATGTTGAGGAGGAAGGACAGCAGCTCGAGCAGCAGCAGGAGGTGGAGGG 3120

Qy  3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACGTCAGACTC 3180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACGTCAGACTC 3180

Qy  3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCAACAGCCCACATTTTCCT 3240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCAACAGCCCACATTTTCCT 3240

Qy  3241 TCCCTAAGCATAGACAATGCCATTTGCCAATAACAAAAGAGAATGCCAATAACAGACTAACTGGT 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 TCCCTAAGCATAGACAATGCCATTTGCCAATAACAAAAGAGAATGCCAATAACAGACTAACTGGT 3300

Qy  3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCGCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCGCAGAGCAAGTGGAAAATGCCAGAGATTG 3360

Qy  3361 TTAAACTTTTCACCCTGACCAGCAGCCACACCCACCAGAGAGAGTGACACGCACGG 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 TTAAACTTTTCACCCTGACCAGCAGCCACACCCACCAGAGAGAGTGACACGCACGG 3420

Qy  3421 AGTGACCTGCAGGGCAGTGGAATTGACCAGCAGGGATTAGTGATGAGCAAGAAAG 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 AGTGACCTGCAGCGCGAGTGGAATTGACCAGCAGGGATTAGTGATGAGCAAGAAAG 3480

Qy  3481 ACAGATTCATTCAAGGGCAGTTCAAGGGCAGTTCAAGGGCAGTTATAGTCCACGTGATCCTGG 3540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 ACAGATTCATTCAAGGGCAGTTCAAGGGCAGTTCAAGGGCAGTTATAGTCCACGTGATCCTGG 3540

Qy  3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAGTCGGGAGA 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGAAAAAATCAGTTCAAGGGAGTCGGGAGA 3600
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Qy    61 TCCTATAAACTGTATAGCCTCCCATTCGGATGGTATGTCTTTGGCAGGATGATAAAGAATCA 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TCCTATAAACTGTATAGCCTCCCATTCGGATGGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy   121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAAGTGTCTGTCTGCTCTCTATTTTAGTGA 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAAGTGTCTGTCTGCTCTCTATTTTAGTGA 180

Qy   181 CAGATGTTGCTCCTGACAGAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CAGATGTTGCTCCTGACAGAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy   241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGCACTGCCCAAGGAAAAATGCCAG 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGCACTGCCCAAGGAAAAATGCCAG 300

Qy   301 GAGAGCAAATGATGAAGAAAATAAACTTTCCCTTGTTTAATTCAGGAAAAAATG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GAGAGCAAATGATGAAGAAAATAAACTTTCCCTTGTTTAATTCAGGAAAAAATG 360

Qy   361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAACAGCTCAGAAATTGG 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAACAGCTCAGAAATTGG 420

Qy   421 TAATTAAGTATTTGTTCCTTGGGAAGACACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TAATTAAGTATTTGTTCCTTGGGAAGACACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy   481 AAACGTCAAAGCATGATCAGATCCAAAGTGATTATTTATTTTAAAAACCAGAT 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AAACGTCAAAGCATGATCAGATCCAAAGTGATTATTTATTTTAAAAACCAGAT 540

Qy   541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAGGACATAACAATAAC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAGGACATAACAATAAC 600

Qy   601 AGCAAAATCAAAATTCCGCAAAATGGGGACTGGAGAAAATGGGGACTGGAAAGCTTTCATAAC 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AGCAAAATCAAAATTCCGCAAAATGGGGACTGGAGAAAATGGGGACTGGAAAGCTTTCATAAC 660

Qy   661 AGTGATTAGGCAGTTGACCATGTTCGCAACATGTCCCCGTCTATACCAGGGAACACGGAACAAAA 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGTGATTAGGCAGTTGACCATGTTCGCAACATGTCCCCGTCTATACCAGGGAACACGGAACAAAA 720

Qy   721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAGAAAACTGAGAGCAAAACAAAA 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAGAAAACTGAGAGCAAAACAAAA 780

Qy   781 GACATGTTAAAAGGCAACCAGACAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GACATGTTAAAAGGCAACCAGACAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy   841 GGGACCCTGAGGCCAGTTTGCCTTTAGGAAGGCCAGTTTCTTAAGGAATCTTAAGAAACTC 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GGGACCCTGAGGCCAGTTTGCCTTTAGGAAGGCCAGTTTCTTAAGGAATCTTAAGAAACTC 900

Qy   901 TTGAAAGATCATGAATTTTAACCATTTTAATAAAACAAATATGCGATGCATAAATCAG 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TTGAAAGATCATGAATTTTAACCATTTTAATAAAACAAATATGCGATGCATAAATCAG 960

Qy   961 TTTAGACATGGGTCCCAATTTTATAAAGTCCCAGCTCC 1020
         ||||||||||||||||||||||||||||||||||||||
Db   961 TTTAGACATGGGTCCCAATTTTATAAAGTCCCAGCTCC 1020

Qy  1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTCAGAATGATC 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTCAGAATGATC 1080

Qy  1081 TGTCATAGCCCTCACACACAGCCCGATGTGTCTGACCTACAACCATCTACAACCCAA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 TGTCATAGCCCTCACACACAGCCCGATGTGTCTGACCTACAACCATCTACAACCCAA 1140
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Db  4680 ATGCAAGACTGAAATTAGAGAAAGTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGGT 4739
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4740 GAGGGGGGAAATCTGCCGCTTCATAGGAGTGAATGCTCTCCCCTGGAGCAGCCGTAGGTGCTGT 4799
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4740 GAGGGGGGAAATCTGCCGCTTCATAGGAGTGAATGCTCTCCCCTGGAGCAGCCGTAGGTGCTGT 4799

Qy  4800 CCTTGTGTTCTGGCTGGCTGTGTTATTTTTCTGTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4800 CCTTGTGTTCTGGCTGGCTGTGTTATTTTTCTGTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859

Qy  4860 TGGATCTCCAGTTCCTACAGTAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4860 TGGATCTCCAGTTCCTACAGTAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919

Qy  4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979

Qy  4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039

Qy  5040 ATAGGAACTATTATTGGGGTATGGTGCATAAATTGGGATGTTCATTTAAAAGAAACT 5099
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5040 ATAGGAACTATTATTGGGGTATGGTGCATAAATTGGGATGTTCATTTAAAAGAAACT 5099

Qy  5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTTGCTCGGCAGCCTGAAGCGCAACCC 5159
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTTGCTCGGCAGCCTGAAGCGCAACCC 5159

Qy  5160 CCCTGTGCACAGCCCCACCCAGCCTCAGTGCTCTTCCCCATGAAGGGCT 5219
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  5160 CCCTGTGCACAGCCCCACCCAGCCTCAGTGCTCTTCCCCATGAAGGGCT 5219

Qy  5220 GGCTCCCCAGTATATATAAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5220 GGCTCCCCAGTATATATAAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
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RESULT 9
US-10-244-633-1
; Sequence 1, Application US/10244633
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 07425.0057.US01
; CURRENT APPLICATION NUMBER: US/10/244,633
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US/09/306,828
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/227,881
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 1
; LENGTH: 5300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-633-1

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  Query Match        99.5%;  Score 5246.4;  DB 43;  Length 5300;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 5269;  Conservative  0;  Mismatches  0;  Indels  2;  Gaps  2;

Qy     1 ATCTTTGTTCAGTTACCTCAGGGCTATTATGAAATGAAATAACCAATGTGAAAG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATCTTTGTTCAGTTACCTCAGGGCTATTATGAAATGAAATAACCAATGTGAAAG 60
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Qy   1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGTCCATTACAACTGCCACCTCCCC 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGTCCATTACAACTGCCACCTCCCC 1200

Qy   1201 TGTGCAGCCATCCGCTCCCGCTCTCCCCACTCTAGACTTCTGACTTCTGCATCACCGATGT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TGTGCAGCCATCCGCTCCCGCTCTCCCCACTCTAGACTTCTGACTTCTGCATCACCGATGT 1260

Qy   1261 TACAGCCAGAAGTCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TACAGCCAGAAGTCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy   1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy   1381 CGGGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CGGGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy   1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGAGTTGATCCACCCACCTC 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGAGTTGATCCACCCACCTC 1500

Qy   1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCCCGCCCGGCCAAGGTCAGTGT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCCCGCCCGGCCAAGGTCAGTGT 1560

Qy   1561 TTAATAAGGAATAACTTGAATGTTTACTAAACCAACAGGGAAAACAGACAAAAGCTGTGA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TTAATAAGGAATAACTTGAATGTTTACTAAACCAACAGGGAAAACAGACAAAAGCTGTGA 1620

Qy   1621 TAATTTCAGGGATTCTTGGGATGGGAATGGTCCATGAGCTGCCATGGTGCCTAGTCCCAGAC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TAATTTCAGGGATTCTTGGGATGGGAATGGTCCATGAGCTGCCATGGTGCCTAGTCCCAGAC 1680

Qy   1681 CACTGGTTCCTCATCACTTTCTTCCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CACTGGTTCCTCATCACTTTCTTCCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy   1741 CACCATTGTCTTTTGTGGTAAGCCTCCACATCGTTACTGAAAATAAGAGTATACATAAACTAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CACCATTGTCTTTTGTGGTAAGCCTCCACATCGTTACTGAAAATAAGAGTATACATAAACTAG 1800

Qy   1801 TTCCATTTGGGCCATCGTGTGTGTGTGTGGAATGCTGCTCGTTCATCCAGGCATTCATTGACAATT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 TTCCATTTGGGCCATCGTGTGTGTGTGTGGAATGCTGCTCGTTCATCCAGGCATTCATTGACAATT 1860

Qy   1861 TGAAGCCCCGGCAGAGTTTCCTCTCCAGCTGGGGAGGCCCTGCGAAGCACCCGGGTCC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TGAAGCCCCGGCAGAGTTTCCTCTCCAGCTGGGGAGGCCCTGCGAAGCACCCGGGTCC 1920

Qy   1921 TGGGTGTCCTGAGCGCAACCTGCCAGCCTCCAGCTGCCACTCGTTGTTGTTATCACTCTCTAGG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGGGTGTCCTGAGCGCAACCTGCCAGCCTCCAGCTGCCACTCGTTGTTGTTATCACTCTCTAGG 1980

Qy   1981 GACCTGTTGCTTTCTATTTCTGTGTGTGTGTGTGTGGACTCGTTCATTCAGGCGAAGAATTAAATAGCCA 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 GACCTGTTGCTTTCTATTTCTGTGTGTGTGTGTGTGGACTCGTTCATTCAGGCGAAGAATTAAATAGCCA 2040

Qy   2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy   2101 CCTACCTTCGTCGAGGTGACAGTTTCTCATGAAGAGACGTGCAGAGAAGAAGAAATTAATAGCCA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCTACCTTCGTCGAGGTGACAGTTTCTCATGAAGAGACGTGCAGAGAAGAAGAAATTAATAGCCA 2160

Qy   2161 GCCAACTTAAACCCAGTCGACAGTTGCTGAAAGAAGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GCCAACTTAAACCCAGTCGACAGTTGCTGAAAGAAGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy   2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCTGCTGCCTCCATCGTGCCGCTGGCC 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCTGCTGCCTCCATCGTGCCGCTGGCC 2280

Qy   2281 CCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCTCCATCAGTCAGTCGACTCACAGCGTCGCTGGCCT 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCTCCATCAGTCAGTCGACTCACAGCGTCGCTGGCCT 2340

Qy   2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGACTCCTTGGCTCCAGGCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGACTCCTTGGCTCCAGGCT 2400

Qy   2401 CCAGAAAGGAAATGAGAGGGAAACTAGTCAACTAGTCTAACGGACGAATCTGGAGGGACCAGTGTTTC 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGACGAATCTGGAGGGACCAGTGTTTC 2460

Qy   2461 CTCAGAGGGAAAGGGGCCTCAGGACGTCGAGCGGGTGCTGAAAGGCAGAAGGTGAAAGGGCAAGGCGAG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CTCAGAGGGAAAGGGGCCTCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520

Qy   2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGCTGAAAGGGCAAGGCTGAA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGCTGAAAGGGCAAGGCTGAA 2580

Qy   2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGTGGGAGTTTTTCCGTTGCTTCCTGTGAGC 2640

Qy   2641 CTTTTTATCTTTCTCTGCTTCTCTGCTTGGAGCAGAGAAGTCTCATTTCATGAACGGGATGCAGTTTC 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 CTTTTTATCTTTCTCTGCTTCTCTGCTTGGAGCAGAGAAGTCTCATTTCATGAACGGGATGCAGTTTC 2700

Qy   2701 ATAAAGTACAGTGTTAAAATTCCAGGGTGTGCATGGGCAGAAGGCAGGAGGTGAAAGGCCTTTAT 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 ATAAAGTCAGTGTTAAAATTCCAGGGTGTGCATGGGCAGAAGGCAGGAGGTGAAAGGCCTTTAT 2760

Qy   2761 TTAATGGAATATAGGAAGCAGCTCATTTCCTAGGCCGTTAATTCACGGAGAAGTGAC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TTAATGGAATATAGGAAGCAGCTCATTTCCTAGGCCGTTAATTCACGGAGAAGTGAC 2820

Qy   2821 TGGAGTCTTTCTTCTTCATGTCTTCTCGGGCAACTACTACTCAGCCCTGTGTGGGGACTTGGCTTA 2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TGGAGTCTTTCTTCTTCATGTCTTCTCGGGCAACTACTACTCAGCCCTGTGTGGGGACTTGGCTTA 2880

Qy   2881 TGCAAGACGGTGAAAACCTTGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTGGTTCTGTCTCGTGCCATT 2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 TGCAAGACGGTGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTGGTTCTGTCTCGTGCCATT 2940

Qy   2941 GGTTGGCTGTGCGACCCGGCAAGTGGGGTTGCGAACGCACCCGGGTCC 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 GGTTGGCTGTGCGACCCGGCAAGTGGGGTTGCGAACGCACCCGGGTCC 3000

Qy   3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGTGTTCGTGAACACTTCCCTGATTCTCTGTGAGGGG 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGTGTTCGTGAACACTTCCCTGATTCTCTGTGAGGGG 3060

Qy   3061 GGATGTTGAGAGGGAGGAGGAGCGAGAGCAGAGCTGAGCTGAGCTGAGCCACAGGGTGGAGGG 3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 GGATGTTGAGAGGGAGGAGGAGCGAGAGCAGAGCTGAGCTGAGCTGAGCCACAGGGTGGAGGG 3120

Qy   3121 GGACAGGAAGGCAGGCAGGCAGCCAGAAGTCGGGTGCTCCTCCATCAGTCGATCACGTCAGACTC 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGACAGGAAGGCAGGCAGGCAGCCAGAAGTCGGGTGCTCCTCCATCAGTCGATCACGTCAGACTC 3180

Qy   3181 CAGGACCGAGAGCCACACAATGCTCAGGAAAGTCAATGACCAACCACAATTTTCCT 3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CAGGACCGAGAGCCACACAATGCTCAGGAAAGTCAATGACCAACCACAATTTTCCT 3240

Qy   3241 TCCCTAAGCATAGACAATGACATTTGCCAATAACCAAAAGAATGCAGAGACTAACTGT 3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TCCCTAAGCATAGACAATGACATTTGCCAATAACCAAAAGAATGCAGAGACTAACTGT 3300

Qy   3301 GGTAGCTTTGCTTGGCATTCAAAAACTGGGCACGAGTTGAAATGGGAAATGCCAGAGATTG 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GGTAGCTTTGCTTGGCATTCAAAAACTGGGCACGAGTTGAAATGGGAAATGCCAGAGATTG 3360

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Qy  3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCACCCCACGCACTGCTGACACGCACG 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCACCCCACGCACTGCTGACACGCACG 3420

Qy  3421 AGTGACCTGCGCAGCGCCAGGGGCGAGGAGAGAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540

Qy  3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAATCAGTTCAAGGGAAGTCGGGGAGA 3600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAATCAGTTCAAGGGAAGTCGGGGAGA 3600

Qy  3601 CCTGATTTCTAATACTATATTTTTCCTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
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Qy  3661 GTAGTAACTGAGGCGTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780

Qy  3781 TAAAGCCAAACAGATTCTTAGAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTGAAAAAT 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 TAAAGCCAAACAGATTCTTAGAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTGAAAAAT 3840

Qy  3841 CATTTCAGCGATGTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 CATTTCAGCGATGTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

Qy  3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGCGTCAACTGCACGAACCAATCAAA- 3959
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGCGTCAACTGCACGAACCAATCAAAT 3960

Qy  3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTCTCCACATCTGAGGTGAGTCGTCGCCAGCGG 4019
         ||||||||||||||||||||||||||||||||||||||||     ||||||||||||||
Db  3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTCTCCAC-TCTCGAGGTGAGTCGTCGCCAGGG 4019

Qy  4020 CAGTTTGGAAATATTTACTTCACAAGTATTGGTTGTTGGTATTAACAACATAAAG 4079
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Qy  4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139

Qy  4140 TTTATTGGCTATTGCCATTGCTTTTTGTTTTTTGTTCTTTTTCTCTTTTGGGTTTAATGTAAAGCA 4199
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4140 TTTATTGGCTATTGCCATTGCTTTTTGTTTTTTGTTCTTTTTCTCTTTTGGGTTTAATGTAAAGCA 4199

Qy  4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259

Qy  4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGGCCATAA 4319
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Qy  4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
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Db  4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379

Qy  4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
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Db  4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
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Qy  4440 ACTTTGAAATTAGACCTCCTGCTGGATCTCTGTTTTTAACATATTAATAAAACATGTTTAA 4499
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4440 ACTTTGAAATTAGACCTCCTGCTGGATCTCTGTTTTTAACATATTAATAAAACATGTTTAA 4499

Qy  4500 AATTTGATATTTGATAATCATATTCATTATCATTGTTTCCTTGTAATCTATATTT 4559
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4500 AATTTGATATTTGATAATCATATTCATTATCATTGTTTCCTTGTAATCTATATTT 4559

Qy  4560 TATATATTTGAAAAACATCTTTCTGAGAAGAGTCCCCAGATTCACCAATGAGGTTCTTG 4619
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4560 TATATATTTGAAAAACATCTTTCTGAGAAGAGTCCCCAGATTCACCAATGAGGTTCTTG 4619

Qy  4620 GCATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGCTGTGCCTGAG 4679
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4620 GCATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGCTGTGCCTGAG 4679

Qy  4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTGTTTTAAAGCTAGGGGT 4739
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTGTTTTAAAGCTAGGGGT 4739

Qy  4740 GAGGGGGGAAATCTGCCGTTCTATAGGAATGCTCTCCCTGGAGCGTGGTAGGGTGCTGT 4799
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4740 GAGGGGGGAAATCTGCCGTTCTATAGGAATGCTCTCCCTGGAGCGTGGTAGGGTGCTGT 4799

Qy  4800 CCTTGTGTTCTGGGCTGGCTGTTATTTTTCTCGTCCTGTCTTAAAGGACTTGTT 4859
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4800 CCTTGTGTTCTGGGCTGGCTGTTATTTTTCTCGTCCTGTCTTAAAGGACTTGTT 4859

Qy  4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGCACAGTGCAGGTTCCAATGAGTTTGCAGA 4919
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGCACAGTGCAGGTTCCAATGAGTTTGCAGA 4919

Qy  4920 GTGAATGAAATATAAACTAGAAATATCCTGTTGAAATCAGCACACCAGTCCTG 4979
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4920 GTGAATGAAATATAAACTAGAAATATCCTGTTGAAATCAGCACACCAGTCCTG 4979

Qy  4980 GTGTAAGTGTGTACGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGAGAT 5039
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4980 GTGTAAGTGTGTACGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGAGAT 5039

Qy  5040 ATAGGAACTATTATTGGGGTATGGGGTATGGGGTGCATAAATTGGATGTTCTTTTAAAAGAAACT 5099
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5040 ATAGGAACTATTATTGGGGTATGGGGTATGGGGTGCATAAATTGGATGTTCTTTTAAAAGAAACT 5099

Qy  5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGCGAAGGCAACCC 5159
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGCGAAGGCAACCC 5159

Qy  5160 CCCTGTGCACAGCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCATGAAGGGCT 5219
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5160 CCCTGTGCACAGCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCATGAAGGGCT 5219

Qy  5220 GGCTCCCCAGTATATATAAATATATAAACCTCTCTGGAGCTCGGGCCATGAGCCAGCAAGG 5271
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5220 GGCTCCCCAGTATATATAAATATATAAACCTCTCTGGAGCTCGGGCCATGAGCCAGCAAGG 5271
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;  LENGTH: 5300
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-741-339-1

Query Match      99.5%;  Score 5246.4;  DB 61;  Length 5300;
Best Local Similarity  99.9%;  Pred. No. 0;
Matches  5269;  Conservative  0;  Mismatches  0;  Indels  2;  Gaps  2;

Qy      1  ATCTTGTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  ATCTTGTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG  60

Qy     61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCGATGATAAAGAATCA  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCGATGATAAAGAATCA  120

Qy    121  GGAAGAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGTCTATTTTAGTGA  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GGAAGAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGTCTATTTTAGTGA  180

Qy    181  CAGATGTGTGCTCCTGACAGAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  CAGATGTGTGCTCCTGACAGAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC  240

Qy    241  CATCAAACAGAGAGCTAAGAAACAGAGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  CATCAAACAGAGAGCTAAGAAACAGAGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG  300

Qy    301  GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTAATTCAGGAAAAAATG  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTAATTCAGGAAAAAATG  360

Qy    361  ATGGAGGACCAAAATCAATGATTAAGGAAACAGCTCAGAAAAAGATGTTTCCAAATTGG  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  ATGGAGGACCAAAATCAATGATTAAGGAAACAGCTCAGAAAAAGATGTTTCCAAATTGG  420

Qy    421  TAATTAAGTATTTGTTCCTTGGGGAAGAGACCTCCATGTGAGCTTGATGGGAAATGGGAA  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  TAATTAAGTATTTGTTCCTTGGGGAAGAGACCTCCATGTGAGCTTGATGGGAAATGGGAA  480

Qy    481  AAACGTCAAAAGCATGATCAGATCCCAAAGTGGATTATTATTTAAAACCAGAT  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  AAACGTCAAAAGCATGATCAGATCCCAAAGTGGATTATTATTTAAAACCAGAT  540

Qy    541  GGCATCACTCTGGGAGGCAAGTTCAGGAAGTCATGTTAGGACACATAACAATAAC  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GGCATCACTCTGGGAGGCAAGTTCAGGAAGTCATGTTAGGACACATAACAATAAC  600

Qy    601  AGCAAAATCAAAATTCCGACAAATTCGGAGGAGGAAATGGGGACTGGGAAAGCTTCATAAAC  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  AGCAAAATCAAAATTCCGACAAATTCGGAGGAGGAAATGGGGACTGGGAAAGCTTCATAAAC  660

Qy    661  AGTGATTAGGCAGTTGACCATGTTCGCAACAGTTCCTTTAGGGAGTTCTTAAGGAACTC  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  AGTGATTAGGCAGTTGACCATGTTCGCAACAGTTCCTTTAGGGAGTTCTTAAGGAACTC  720

Qy    721  ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATAATGAAAAACTGAGAGCAAACAAAA  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATAATGAAAAACTGAGAGCAAACAAAA  780

Qy    781  GACATGGTTAAAAGGCAACAGAACATTGTGAGCCAGTTTCTTAGGAATCTTAAGAAACTC  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GACATGGTTAAAAGGCAACAGAACATTGTGAGCCAGTTTCTTAGGAATCTTAAGAAACTC  840

Qy    841  GGGACCCTGAGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAGGAATATAAAACAAATATCGCATGATGCATGAATCAG  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  GGGACCCTGAGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAGGAATATAAAACAAATATCGCATGATGCATGAATCAG  900

Qy    901  TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATGAATCAG  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATGAATCAG  960

Qy    961  TTTAGACATGGTCCCAATTTTATAAAGTCAGGCATACAACAAGGATAACGTGTCCCAGCTCC  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TTTAGACATGGTCCCAATTTTATAAAGTCAGGCATACAACAAGGATAACGTGTCCCAGCTCC  1020

Qy   1021  GGATAGTTCAGAAATCATTAGAAAATCACTGTGTCCCATCCTAACTTTTCAGAATGATC  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  GGATAGTTCAGAAATCATTAGAAAATCACTGTGTCCCATCCTAACTTTTCAGAATGATC  1080

Qy   1081  TGTCATAGCCCTCACACAGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  TGTCATAGCCCTCACACAGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA  1140

Qy   1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCATTACAAATGCCACCTCCC  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCATTACAAATGCCACCTCCC  1200

Qy   1201  TGTGCAGCCCATCCCGTCCACAGGAGTCTCCCCACTCTCGACTTCTGCATCACGATGT  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  TGTGCAGCCCATCCCGTCCACAGGAGTCTCCCCACTCTCGACTTCTGCATCACGATGT  1260

Qy   1261  TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTCTTCACACCTGTCTCACCTGTATGCTCTAC  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTCTTCACACCTGTCTCACCTGTATGCTCTAC  1320

Qy   1321  ACCTGAGCTCACTGCAACCTCTGCCTCCGTCTTCAAGCAATTCTCCGTCTCAGCCTCC  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  ACCTGAGCTCACTGCAACCTCTGCCTCCGTCTTCAAGCAATTCTCCGTCTCAGCCTCC  1380

Qy   1381  CGCGTAGCTCGGACTACAGGCGCACCGCGGCTAATTTTGTATTGTTAGTAGAGATGGG  1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CGCGTAGCTCGGACTACAGGCGCACCGCGGCTAATTTTGTATTGTTAGTAGAGATGGG  1440

Qy   1441  GTTTCACCATTAGCCGCGCTGGTCTTGAACTCCTCAGTGATCCCAGGTCAGTGT  1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  GTTTCACCATTAGCCGCGCTGGTCTTGAACTCCTCAGTGATCCCAGGTCAGTGT  1500

Qy   1501  AGCCTCCTAAAGTGCTGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT  1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  AGCCTCCTAAAGTGCTGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT  1560

Qy   1561  TTAATAAGGAATAACTTGAATGGTTACTAAACCAACAGGGAAACAGACAAAAGCTGA  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  TTAATAAGGAATAACTTGAATGGTTACTAAACCAACAGGGAAACAGACAAAAGCTGA  1620

Qy   1621  TAAATTTCAGGGATTCTTGGGATGGGAATGGCCATGAGCTGCCTAGTCCCAGAC  1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  TAAATTTCAGGGATTCTTGGGATGGGAATGGCCATGAGCTGCCTAGTCCCAGAC  1680

Qy   1681  CACTGGTCCTCATCACTTTCTCCCTCATTTCAGGCTAAGCTAAGTTACCATTTTATT  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  CACTGGTCCTCATCACTTTCTCCCTCATTTCAGGCTAAGCTAAGTTACCATTTTATT  1740

Qy   1741  CACCATGCTCTTTGTGTGGTAAGCCTCCACATGTGAAATAAGAGTATACATAAACTAG  1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  CACCATGCTCTTTGTGTGGTAAGCCTCCACATGTGAAATAAGAGTATACATAAACTAG  1800

Qy   1801  TTCCATTTGGGGCCATCGTGTGTGTAGGGGGAGGGGCCATACCCCCAGAGACTCCT  1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  TTCCATTTGGGGCCATCGTGTGTGTAGGGGGAGGGGCCATACCCCCAGAGACTCCT  1860

Qy   1861  TGAAGCCCCCGGCAGAGGTTTCTCTCCAGCCCGTGCCACTGCAAGCACCCGGGGTCC  1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  TGAAGCCCCCGGCAGAGGTTTCTCTCCAGCCCGTGCCACTGCAAGCACCCGGGGTCC  1920

Qy   1921  TGGGTGTCCTGAGCAACCTGGTTTCTTGTTTGTTATCGTCTCTAGG  1980
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  TGGGTGTCCTGAGCAACCTGGTTTCTTGTTTGTTATCGTCTCTAGG  1980

Qy   1981  GACCTGTTGCTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT  2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  GACCTGTTGCTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT  2040

Qy   2041  TATTGAGTACTTATATCTGCCAGACACCAGAGACAGACACCAGAGAATGGTGAGCAAAGCTCACTGC  2100
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; GENERAL INFORMATION:
;   APPLICANT: Morris, David W.
;   APPLICANT: Engelhard, Eric K.
;   TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
;   TITLE OF INVENTION: CANCER
;   FILE REFERENCE: 52945200122
;   CURRENT APPLICATION NUMBER: US/10/087,192
;   CURRENT FILING DATE: 2002-03-01
;   PRIOR APPLICATION NUMBER: US 09/747,377
;   PRIOR FILING DATE: 2000-12-22
;   PRIOR APPLICATION NUMBER: US 09/798,586
;   PRIOR FILING DATE: 2001-03-02
;   NUMBER OF SEQ ID NOS: 2059
; SEQ ID NO 1228
;   LENGTH: 37252
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   SOFTWARE: FastSEQ for Windows Version 4.0
US-10-087-192-1228

Query Match             99.3%;  Score 5232.4;  DB 40;  Length 37252;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 5267;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 3;
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Qy      1  ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAGATAACCAATGTGAAAG  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4731  ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAGATAACCAATGTGAAAG  4790

Qy     61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGGATGATAAAGAATCA  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4791  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGGATGATAAAGAATCA  4850

Qy    121  GGAAGAGGAGTATCCAAGTTAGCCAAGTGTCCAAGTGCTGTGTCTGCTCTTATTTTAGTGA  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4851  GGAAGAGGAGTATCCAAGTTAGCCAAGTGTCCAAGTGCTGTGTCTGCTCTTATTTTAGTGA  4910

Qy    181  CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4911  CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC  4970

Qy    241  CATCAAACAGAGCTAAGAAACAGGAATGAGATGAGGAATGAAAAATGCCAG  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4971  CATCAAACAGAGCTAAGAAACAGGAATGAGATGAGGAATGAAAAATGCCAG  5030

Qy    301  GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTAATTCAGGAAAAAATG  360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5031  GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTAATTCAGGAAAAAATG  5090

Qy    361  ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAGATGTTTCCAAATTGG  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5091  ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAGATGTTTCCAAATTGG  5150

Qy    421  TAATTAAGTATTTGTTCCTTGGGAAGAGAATTCAGGAATGGGAAATGGGAA  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5151  TAATTAAGTATTTGTTCCTTGGGAAGAGAATTCAGGAATGGGAAATGGGAA  5210

Qy    481  AAACGTCAAAAGCATGATCTGATCGATCAGATCCCAAAGTGGATTATTATTTAAAAACCAGAT  540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5211  AAACGTCAAAAGCATGATCTGATCGATCAGATCCCAAAGTGGATTATTATTTAAAAACCAGAT  5270

Qy    541  GGCATCACTCTGGGGAGGCAAGTTCAGGAAGTCATGTTAGCAAGGACATAACAATAAC  600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5271  GGCATCACTCTGGGGAGGCAAGTTCAGGAAGTCATGTTAGCAAGGACATAACAATAAC  5330

Qy    601  AGCAAAATCAAAATTCCGCAAATGCAAATGGGGACTGGGAAAAGCTTTCATAAC  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5331  AGCAAAATCAAAATTCCGCAAATGCAAATGGGGACTGGGAAAAGCTTTCATAAC  5390

Qy    661  AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCAACACCTCCCGTCTATACCAGGGAACACAAAA  720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5391  AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCAACACCTCCCGTCTATACCAGGGAACACAAAA  5450

Qy    721  ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA  780
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Qy  4260  TTGTTTTACCACCTTCTAACTAAATTAACATTTATTCATTGCGAATAGAGCCATAA  4319
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4260  TTGTTTTACCACCTTCTAACTAAATTAACATTTATTCATTGCGAATAGAGCCATAA  4319

Qy  4320  ACTCAAAGTGTAATAACAGTACCTGTGATTTGTCATTACCAATAGAAATCACAGACAT  4379
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4320  ACTCAAAGTGTAATAACAGTACCTGTGATTTGTCATTACCAATAGAAATCACAGACAT  4379

Qy  4380  TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTTATACTCAAAACT  4439
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4380  TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTTATACTCAAAACT  4439

Qy  4440  ACTTTGAAATTAGACCTCCTGGATCTGTTTTTAACATATTAATAATAAAACATGTTTAA  4499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4440  ACTTTGAAATTAGACCTCCTGGATCTGTTTTTAACATATTAATAATAAAACATGTTTAA  4499

Qy  4500  AATTTTGATATATTTGATAATCATATTTCATTATCATATATTGTTTGTTCCTTGTAATCTATATTT  4559
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4500  AATTTTGATATATTTGATAATCATATTTCATTATCATATATTGTTTGTTCCTTGTAATCTATATTT  4559

Qy  4560  TATATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG  4619
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4560  TATATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG  4619

Qy  4620  GCATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGACATTGGTGTGCCTGAG  4679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4620  GCATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGACATTGGTGTGCCTGAG  4679

Qy  4680  ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTGTTTAAAGCTAGGGGT  4739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4680  ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTGTTTAAAGCTAGGGGT  4739

Qy  4740  GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT  4799
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4740  GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT  4799

Qy  4800  CCTTGTGTTCTGGCTGTGTTATTTTTCTCTGTCCCGTCTACGTCTTAAAGGACTTGTT  4859
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4800  CCTTGTGTTCTGGCTGTGTTATTTTTCTCTGTCCCGTCTACGTCTTAAAGGACTTGTT  4859

Qy  4860  TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTTCAGGTTCTCAATGAGTTTGCAGA  4919
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4860  TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTTCAGGTTCTCAATGAGTTTGCAGA  4919

Qy  4920  GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGTGAAATCAGCACACCAGTAGTCCTG  4979
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4920  GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGTGAAATCAGCACACCAGTAGTCCTG  4979

Qy  4980  GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTAAACCAGGTGTAAAACCAGGTGAGAT  5039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4980  GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTAAACCAGGTGTAAAACCAGGTGAGAT  5039

Qy  5040  ATAGGAACTATTATTGGGGTATGGGTGCATAAATTTCTAAGAAATCTTGCTGCCAGGCAACCC  5099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5040  ATAGGAACTATTATTGGGGTATGGGTGCATAAATTTCTAAGAAATCTTGCTGCCAGGCAACCC  5099

Qy  5100  CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAAATCTTGCTGCCAGGCGTGAAGGCAACCC  5159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5100  CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAAATCTTGCTGCCAGGCGTGAAGGCAACCC  5159

Qy  5160  CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCGTCTTCTTCCCCATGAAGGGCT  5219
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5160  CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCGTCTTCTTCCCCATGAAGGGCT  5219

Qy  5220  GGCTCCCCAGTATATAAACCTCTCTGGAGCTCGGCCAGGCCAGGCAAGG  5271
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5220  GGCTCCCCAGTATATAAACCTCTCTGGAGCTCGGCCAGGCCAGGCAAGG  5271
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RESULT 11
US-10-087-192-1228
; Sequence 1228, Application US/10087192
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Qy 4020 CAGTTTGGAAATATTTACTTCACAAGTATTGTGTTGGTATTAACAACATAAAG 4079
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8750 CAGTTTGGAAATATTTACTTCACAAGTATTGTGTTGGTATTAACAACATAAAG 8809

Qy 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTAAAGTTACTTCTGACAGTTTGGTATA 4139
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8810 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTAAAGTTACTTCTGACAGTTTGGTATA 8869

Qy 4140 TTTATTGGCTATTGCCATTTGCTTTTGTTTTTGTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8870 TTTATTGGCTATTGCCATTTGCTTTTGTTTTTGTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 8929

Qy 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTGAATGGAGGAAAAAATTACATTT 4259
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8930 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTGAATGGAGGAAAAAATTACATTT 8989

Qy 4260 TTGTTTTACCACCTTCTAACTAAATTAACATTTTATTCATTTTATTCGCAAATAGAGCCCATAA 4319
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8990 TTGTTTTACCACCTTCTAACTAAATTAACATTTTATTCATTTTATTCGCAAATAGAGCCCATAA 9049

Qy 4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAATCACAGACAT 4379
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9050 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAATCACAGACAT 9109

Qy 4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9110 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 9169

Qy 4440 ACTTTGAAATTAGACCTTGTTGTTAACATATTTAATTAATTAAAACATGTTTAA 4499
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9170 ACTTTGAAATTAGACCTTGTTGTTAACATATTTAATTAATTAAAACATGTTTAA 9229

Qy 4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATTCTATATTT 4559
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9230 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATTCTATATTT 9289

Qy 4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTCCCAGATTCACCAGATTGAGGTTCCTG 4619
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9290 TATATATTTGAAAACATCTTTCTGAGAAGAGTCCCAGATTCACCAGATTGAGGTTCCTG 9349

Qy 4620 GCATGCACACACAGAGAACTGATTTAGAGGCTAACATTGACATTGGTCCTGAG 4679
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9350 GCATGCACACACAGAGAACTGATTTAGAGGCTAACATTGACATTGGTCCTGAG 9409

Qy 4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAGCTAGGGGT 4739
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9410 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTAAAGCTAGGGGT 9469

Qy 4740 GAGGGGGAAATCTGCGCCGCTTCATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9470 GAGGGGGAAATCTGCGCCGCTTCATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 9529

Qy 4800 CCTTGTGTTCTCGCTGGCTGGCTGTGTATTTTCTGTCCGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9530 CCTTGTGTTCTCGCTGGCTGGCTGTGTATTTTCTGTCCGTCCCTGCTACGTCTTAAAGGACTTGTT 9589

Qy 4860 TGGATCTCCAGTTCCTAGCATAGTGGGTATGGGTGCATAAATTGGGATGTTCTTTTGCAGA 4919
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9590 TGGATCTCCAGTTCCTAGCATAGTGGGTATGGGTGCATAAATTGGGATGTTCTTTTGCAGA 9649

Qy 4920 GTGAATGGAAATATAAACTAGAACATCCTTGTTGTGTGTGTAAAACCAGTAGTCCTG 4979
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9650 GTGAATGGAAATATAAACTAGAACATCCTTGTTGTGTGTGTAAAACCAGTAGTCCTG 9709

Qy 4980 GTGTAAGTGTGTGTACGTGTGTGTAC--GTGTGTGTGTGTGTGTGTGTGGAGAT 5039
         ||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db 9710 GTGTAAGTGTGTGTAC--GTGTGTGTGTGTGTGTGTGTGTGTGGAGAT 9767

Qy 5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTTAAAAAGAAACT 5099
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9768 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTTAAAAAGAAACT 9827

Qy 5100 CCAAACAGACTTCTGAAGGTTATTTTCTAAGAAATCTTGCTCGCGGCAGCCTGAAGGCAACCC 5159

Qy 2941 GGTTGGCTGTGTGCGACCGTGGGCAAGTGTCTTCTTCCCTCGGGCCATAGTGTTCTTCTGCT 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7671 GGTTGGCTGTGTGCGACCGTGGGCAAGTGTCTTCTTCCCTCGGGCCATAGTGTTCTTCTGCT 7730

Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTCGTGAACACTTCCCTGTGAATTCTCTGTGAGGGG 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7731 ATAAAGACCCTTGCAGCTCTCGTGTTCTCGTGAACACTTCCCTGTGAATTCTCTGTGAGGGG 7790

Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGAGCAGCTGAGCAGCTGAGCAGGGGAGGTGGAGGG 3120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7791 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGAGCAGCTGAGCAGCTGAGCAGGGGAGGTGGAGGG 7850

Qy 3121 GGACACGGAAGGCAGGCAGAAGCTGGGTGCTGTCCATCAGTCCTCACTCACTGATCACACTC 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7851 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTGTCCATCAGTCCTCACTCACTGATCACAGACTC 7910

Qy 3181 CAGGACCGAGAGCCACAAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCCACATTTTCCT 3240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7911 CAGGACCGAGAGCCACAAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCCACATTTTCCT 7970

Qy 3241 TCCCTTAAGCAATAGACAATGGCATTTGCCAATAACCAAAAGAATGCAGAGACTAACTGGT 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7971 TCCCTTAAGCAATAGACAATGGCATTTGCCAATAACCAAAAGAATGCAGAGACTAACTGGT 8030

Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAAGTGCAAGCAAGTGGAAAATGCCAGAGATTG 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8031 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAAGTGCAAGCAAGTGGAAAATGCCAGAGATTG 8090

Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGTGCTGCTGCTGCAGCACGG 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8091 TTAAACTTTTCACCCTGACCAGCACCCCACGTGCTGCTGCTGCAGCACGG 8150

Qy 3421 AGTGACCTGCAGCGCGCGAGGGGAGGAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8151 AGTGACCTGCAGCGCGCGAGGGGAGGAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 8210

Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCAGTATAGTCCACGTGATCCTGG 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8211 ACAGATTCATTCAAGGGCAGTGGGAATTGACCAGTATAGTCCACGTGATCCTGG 8270

Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGGAGA 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8271 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGGAGA 8330

Qy 3601 CCTGATTTCTAATACTATATTTTCCTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8331 CCTGATTTCTAATACTATATTTTCCTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 8390

Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTCTCTGT 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8391 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTCTCTGT 8450

Qy 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTCTTTAACAGGAAGAAACATTCCTAAGAG 3780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8451 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTCTTTAACAGGAAGAAACATTCCTAAGAG 8510

Qy 3781 TAAAGCCAAACAGATTCAAGCCTCAGGCCTTTGGTTTTTTGAAAAT 3840
         ||||||||||||||||||||||||||||||||||||||||||||||
Db 8511 TAAAGCCAAACAGATTCAAGCCTCAGGCCTTTGGTTTTTTGAAAAT 8570

Qy 3841 CATTTCAGCGGATGTTTACTATGTCTTGAAATGCTCAAGTTCAGGCTTAAGTGTCGGCTTACCCTTTGGTCAGCTG 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8571 CATTTCAGCGGATGTTTACTATGTCTTGAAATGCTCAAGTTCAGGCTTAAGTGTCGGCTTACCCTTTGGTCAGCTG 8630

Qy 3901 TAAACAAACACCCCAGTTGTAAATGTCTTAACTGCAGAAGCTTAACTGCAGAACCAATCAAA- 3959
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8631 TAAACAAACACCCCAGTTGTAAATGTCTTAACTGCAGAAGCTTAACTGCAGAACCAATCAAAT 8690

Qy 3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTTCTCCAC-TCTCGGAGGTGAGTCTGCCAGGG 4019
         |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db 8691 AAGAATAGAATCTTTAGAGCAAACTGTGTTTTCTCCAC-TCTCGGAGGTGAGTCTGCCAGGG 8749

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Db  9828  ||||||||||||||||||||||||||||||||||||||||||||||
          CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTCTGCTGGCAGCGTGAAGGCAACCC  9887

Qy  5160  CCCTGTGCACAGCCCACCCAGCCTCAGGTGGCCACCTCGTCTTCCCCCATGAAGGGCT  5219
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  9888  CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCGTCTTCCCCCATGAAGGGCT  9947

Qy  5220  GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCGCAGCCAAGG  5271
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  9948  GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCCAAGG  9999

RESULT 12
US-08-938-669-2
; Sequence 2, Application US/08938669
; GENERAL INFORMATION:
;   APPLICANT: Nguyen, Thai D.
;   APPLICANT: Polansky, Jon R.
;   TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
;   TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND RELATED DISEASE
;   NUMBER OF SEQUENCES: 32
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Howrey & Simon
;     STREET: 1299 Pennsylvania Avenue, N.W.
;     CITY: Washington
;     STATE: DC
;     COUNTRY: USA
;     ZIP: 20004-2402
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/938,669
;     FILING DATE:
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/791,154
;     FILING DATE: 28-JAN-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Sira, Serge
;     REGISTRATION NUMBER: 39,445
;     REFERENCE/DOCKET NUMBER: 07425-0034
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 202 383-6857
;     TELEFAX: 202 383-6610
;     TELEX:
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 5304 base pairs.
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
US-08-938-669-2

Query Match    99.1%;  Score 5224.4;  DB 19;  Length 5304;
Best Local Similarity  99.8%;  Pred. No. 0;
Matches 5264;  Conservative  0;  Mismatches  6;  Indels  6;  Gaps  3;

Qy   1  ATCTTTGTTCAGTTACCTCAGGCTATTATCCGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1  ATCTTTGTTCAGTTACCTCAGGCTATTATCCGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG  60

Qy  61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA  120

Qy 121  GGAAGAGGAGTATCCACGTTAGCCAAGTGTCCAAGGCTGTGTGTCTTATTTTAGTGA  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121  GGAAGAGGAGTATCCACGTTAGCCAAGTGTCCAAGGCTGTGTGTCTTATTTTAGTGA  180
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Qy  181  CAGATGTTGCTCCTGACAGAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  CAGATGTTGCTCCTGACAGAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC  240

Qy  241  CATCAAACAGGAGCTAAGAACACAGGAATGAGATGGGCACTTGCCCAGGAAAATGCCAG  300
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  CATCAAACAGGAGCTAAGAACACAGGAATGAGATGGGCACTTGCCCAGGAAAATGCCAG  300

Qy  301  GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTAATTTCAGGAAAAAATG  360
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTAATTTCAGGAAAAAATG  360

Qy  361  ATGAGGACCAAAATCAATGAATAAGGAAAAACAGCTCAGAAAAAAGAGTGTTTCCAAATTGG  420
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  ATGAGGACCAAAATCAATGAATAAGGAAAAACAGCTCAGAAAAAAGAGTGTTTCCAAATTGG  420

Qy  421  TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA  480
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA  480

Qy  481  AAACGTCAAAGACATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT  540
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  AAACGTCAAAGACATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT  540

Qy  541  GGCATCACTCTGGGGAGGCAAGTCAGGAAGTCATGTAGCGAAGGACATAACAATAAC  600
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  541  GGCATCACTCTGGGGAGGCAAGTCAGGAAGTCATGTAGCGAAGGACATAACAATAAC  600

Qy  601  AGCAAAATCAAAATTCCGCAAATGCAAATGCGAGGAGGAAAATGGGACTGGGAAAGCTTTCATAAC  660
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  601  AGCAAAATCAAAATTCCGCAAATGCAAATGCGAGGAGGAAAATGGGACTGGGAAAGCTTTCATAAC  660

Qy  661  AGTGATTAGGCAGTTGACCATGTTCGCAACACACTCCCGTCTATACCAGGGAACACAAAA  720
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  661  AGTGATTAGGCAGTTGACCATGTTCGCAACACACTCCCGTCTATACCAGGGAACACAAAA  720

Qy  721  ATTGACTGGGCTAAGCCTGGACTTTCAAGGAGAAATATGAAAAACTGAGAGCAAAACAAAA  780
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  721  ATTGACTGGGCTAAGCCTGGACTTTCAAGGAGAAATATGAAAAACTGAGAGCAAAACAAAA  780

Qy  781  GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA  840
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  781  GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA  840

Qy  841  GGGACCCTGAGGCATTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC  900
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  841  GGGACCCTGAGGCATTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC  900

Qy  901  TTGAAAGATCATGAATTTAACCATTTTAATAAACAAATATGCGATGCATAATCAG  960
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  901  TTGAAAGATCATGAATTTAACCATTTTAATAAACAAATATGCGATGCATAATCAG  960

Qy  961  TTTAGACATGGGTCCCAATTTTATAAGTCAGGCATACAACGTGTGTCCCAGTCTCC  1020
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  961  TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAACGTGTGTCCCAGTCTCC  1020

Qy 1021  GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTTCAGAATGATC  1080
         ||||||||||||||||||||||||||||||||||||||||||||||
Db 1021  GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTTCAGAATGATC  1080

Qy 1081  TGTCATAGCCCTCACACACAGGCCGATGTGTCTGACCTACAACCATCTACAACCAA  1140
         ||||||||||||||||||||||||||||||||||||||||||||||
Db 1081  TGTCATAGCCCTCACACACACAGGCCCGATGTGTCTGACCTACAACCACTACAACCAA  1140

Qy 1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC  1200
         ||||||||||||||||||||||||||||||||||||||||||||||
Db 1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC  1200

Qy 1201  TGTGCAGCCCATCCCGCTCCACAGGAGTCTCCCACTCTAGACTTCTGCATCACGATGT  1260
         ||||||||||||||||||||||||||||||||||||||||||||||
Db 1201  TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCACTCTAGACTTCTGCATCACGATGT  1260

Qy 1261  TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTCACCTACCTGTATGCTCTAC  1320
         ||||||||||||||||||||||||||||||||||||||||||||||
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Qy 4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619

Qy 4620 GCATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGGTGTGCCTGAG 4679
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4620 GCATGCACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGGTGTGCCTGAG 4679

Qy 4680 ATGCAAGACTGAAATTAGAAAGTTCTCCAAAGATACACAGTGTTTAAAGCTAGGGGT 4739
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4680 ATGCAAGACTGAAATTAGAAAGTTCTCCAAAGATACACAGTGTTTAAAGCTAGGGGT 4739

Qy 4740 GAGGGGGAAATCTGCCGCTTCTATAGGAAATGCTCTCCCGGAGCCTGGTAGGGTGCTGT 4799
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4740 GAGGGGGAAATCTGCCGCTTCTATAGGAAATGCTCTCCCGGAGCCTGGTAGGGTGCTGT 4799

Qy 4800 CCTTGTGTTCTGGCTGGCTGTTATTTTCTCTGTCCCTGCCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4859
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4800 CCTTTGTGTTCTGGCTGGCTGTTATTTTCTCTGTCCCTGCCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4859

Qy 4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTGTTGAAATCAGCACCAGTAGTCCTG 4919
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTGTTGAAATCAGCACCAGTAGTCCTG 4919

Qy 4920 GTGAATGAAATATAAACTAGAAATATATCCTTGTTGTTGAAATCAGCACCAGTAGTCCTG 4979
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4920 GTGAATGAAATATAAACTAGAAATATATCCTTGTTGTTGAAATCAGCACCAGTAGTCCTG 4979

Qy 4980 GTGTAAGTGTGTGTAC---GTGTGTGTGTGTGTGTGTGTGTAAACCAGGTGG 5035
        |||||||||||||||| ||||||||||||||||||||||||||||||||
Db 4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAACCAGGTGG 5039

Qy 5036 AGATATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGATGTTCTTTTAAAAGA 5095
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5040 AGATATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGATGTTCTTTTAAAAGA 5099

Qy 5096 AACTCCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCA 5155
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5100 AACTCCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCA 5159

Qy 5156 ACCCCCCTGTGCACAGCCCCACCCAGCCCACCCAGCCCACCCTGTCTTCCCCCATGAAG 5215
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5160 ACCCCCCTGTGCACAGCCCCACCCAGCCCACCCAGCCCACCCTGTCTTCCCCCATGAAG 5219

Qy 5216 GGCTGGCTCCCCAGTATATATAAACCTCTCGAGCCTCGGGGCATGAGGCCAGCAAGG 5271
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5220 GGCTGGCTCCCCAGTATATATAAACCTCTCGAGCCTCGGGGCATGAGGCCAGCAAGG 5275

RESULT 13
US-09-227-881-2
; Sequence 2, Application US/09227881
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis /
; CURRENT APPLICATION NUMBER: US/09/227,881
; CURRENT FILING DATE: 1999-01-11
; EARLIER APPLICATION NUMBER: US 08/938,669
; EARLIER FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 2
; LENGTH: 5304
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-227-881-2

Query Match   99.1%; Score 5224.4; DB 22; Length 5304;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 5264; Conservative 0; Mismatches 6; Indels 6; Gaps 3;

Qy 3481 ACAGATTCATTCAAGGCAGTGGAATTGACCACCAGGGATTATAGTCCACGTGATCCTGG 3540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3481 ACAGATTCATTCAAGGCAGTGGAATTGACCACCAGGGATTATAGTCCACGTGATCCTGG 3540

Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGAAAAAATCAGTTCAAGGGAAGTCGGAGA 3600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGAAAAAATCAGTTCAAGGGAAGTCGGAGA 3600

Qy 3601 CCTGATTTCTAATACTACTATATATTTTCCTTTACAAGCTGAGCAAGCTCGAGCAGCTCACAAG 3660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3601 CCTGATTTCTAATACTACTATATATTTTCCTTTACAAGCTGAGCAAGCTCGAGCAGCTCACAAG 3660

Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTATTAGGAGAACTCTTTTCTCTGT 3720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTATTAGGAGAACTCTTTTCTCTGT 3720

Qy 3721 GGAGTTAGGCAGCACAAGGGCAATCCCGTTCTTCTTTAACAGGAGAGAAAACATTCCTAGAG 3780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3721 GGAGTTAGGCAGCACAAGGGCAATCCCGTTCTTCTTTAACAGGAGAGAAAACATTCCTAGAG 3780

Qy 3781 TAAAGCCAAACAGAGATTCAAGCCTCAGTCTGTTGCTGACTAGTACCCTTTGTCAGCTG 3840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3781 TAAAGCCAAACAGAGATTCAAGCCTCAGTCTGTTGCTGACTAGTACCCTTTGTCAGCTG 3840

Qy 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGTCAGCTG 3900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGTCAGCTG 3900

Qy 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGCTTAACTGCAGAACCAATCAAA- 3959
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3901 TAAACAAACACCCCATTTGTAAATGTCTCAAGTTCAGCTTAACTGCAGAACCAATCAAT 3960

Qy 3960 AAGAATAGAAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGAGGTGAGTCTGCCAGGG 4019
        |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db 3961 AAGAATAGAAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGAGGTGAGTCTGCCAGGG 4019

Qy 4020 CAGTTTGAAATATTTACTTCACAAGTATTGGTGTTGGTATTAACACATAAAG 4079
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4020 CAGTTTGAAATATTTACTTCACAAGTATTGGTGTTGGTATTAACACATAAAG 4079

Qy 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139

Qy 4140 TTTATTGGCTATTGCCATTTGTTTTTGTTTTTTTGTTTTATTGGGTTTATTAATGTAAAGCA 4199
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4140 TTTATTGGCTATTGCCATTTGTTTTTGTTTTTTTGTTTTATTGGGTTTATTAATGTAAAGCA 4199

Qy 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATTTGAATGAGGAAAAAATTACATTT 4259
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATTTGAATGAGGAAAAAAATTACGTTT 4259

Qy 4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCCGAATAGAGCCATAA 4319
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4260 TTATTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCCGAATAGAGCCATAA 4319

Qy 4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379

Qy 4380 TTTATACTATTACAGTTGTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4380 TTTATACTATTACAGTTGTGCAGGTACGTTGTAAGTGAAATATTTATACTCAAAACT 4439

Qy 4440 ACTTTGAAATTAGACCTTCCCTGCTGATCTTGTTTTTTAACATATTAATTAATAAAACATGTTAA 4499
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4440 ACTTTGAAATTAGACCTTCCCTGCTGATCTTGTTTTTTAACATATTAATTAATAAAACATGTTAA 4499

Qy 4500 AATTTTGATATATTTGATAATCATATTTCATTATCATTTCTTTGTTCCTTTGTAATCTATATTT 4559
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4500 AATTTTGATATATTTGATAATCATATTTCATTATCATTTCTTTGTTCCTTTGTAATCTATATTT 4559

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Qy    1  ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAGATAACCAATGTGAAAG   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAGATAACCAATGTGAAAG   60

Qy   61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAGAGAATCA  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAGAATCA  120

Qy  121  GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCGTCTCTTATTTTAGTGA  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  GGAAGAGAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCGTCTCTTATTTTAGTGA  180

Qy  181  CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATAGGTAAATC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATAGTAAATC  240

Qy  241  CATCAAACAGGAGCTAAGAACAGGAATGAGATGGGCACTTGCCCAAGGAAAATGCCAG  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  CATCAAACAGGAGCTAAGAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG  300

Qy  301  GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTAATTTCAGGAAAAAATG  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTAATTTCAGGAAAAAATG  360

Qy  361  ATGAGGACCAAAATCAATGAATAAGGAAAAAGAGCTTCAGAGAAAAAGAGATGTTTCCAAATTGG  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  ATGAGGACCAAAATCAATGAATAAGGAAAAAGAGCTTCAGAGAAAAAGAGATGTTTCCAAATTGG  420

Qy  421  TAATTAAGTATTTGTTCCTTGGGAAGACCTTCCATGTGAGCTTGATGGGAAATGGGAA  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  TAATTAAGTATTTGTTCCTTGGGAAGACCTTCCATGTGAGCTTGATGGGAAATGGGAA  480

Qy  481  AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT  540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT  540

Qy  541  GGCATCACTCTGGGGAGGCAAGTTCAGGATCATGTTAGACAAAGGACATGACAATAAC  600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  GGCATCACTCTGGGGAGGCAAGTTCAGGATCATGTTAGACAAAGGACATGACAATAAC  600

Qy  601  AGCAAAATCAAAATTCCGACAAATGGGGACTGGGAAAATGGGAAAGCTTTCATAAC  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  AGCAAAATCAAAATTCCGACAAATGGGGACTGGGAAAATGGGAAAGCTTTCATAAC  660

Qy  661  AGTGATTAGGCAGTTGACCCATGTTCGCAACACCTCTATACCAGGGAACACACAAA  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  AGTGATTAGGCAGTTGACCCATGTTCGCAACACCTCTATACCAGGGAACACACAAA  720

Qy  721  ATTGACTGGGCTAAGCCTGACTTTGCCTTTAAGTAGTATAAAAACAATATGGCAATAATCAG  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721  ATTGACTGGGCTAAGCCTGACTTTGCCTTTAAGTAGTATAAAAACAATATGGCAATAATCAG  780

Qy  781  GACAATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGAGCAGTGCCCTCAGCA  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781  GACAATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGAGCAGTGCCCTCAGCA  840

Qy  841  GGGACCCCTGAGGCATTTGCCTTTAAGGAAGGCCAGTTTCTTAAGTAGATCATGATGAAATCC  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841  GGGACCCCTGAGGCATTTGCCTTTAAGGAAGGCCAGTTTCTTAAGTAGATCATGATGAAATCC  900

Qy  901  TTGAAAGTACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901  TTGAAAGTACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  960

Qy  961  TTTAGACATGGGTCCCAATTTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961  TTTAGACATGGGTCCCAATTTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy 1021  GGATAAGTCAGAAATCATTAGAAATCAATCACTGTGTCCCCATCCTAACTTTTCAGAATGATC 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021  GGATAAGTCAGAAATCATTAGAAATCAATCACTGTGTCCCCATCCTAACTTTTCAGAATGATC 1080
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Qy 1081  TGTCATAGCCCTCACACACAGCCCGATGTGTCTGACCACACTCACAACCCAA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081  TGTCATAGCCCTCACACACAGCCCGATGTGTCTGACCACACTCACAACCCAA 1140

Qy 1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTGAGGTCCCATTACAAATGCCACCTCCCC 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141  GTGCCTCAACCATTGTTAACGTGTCATCTCAGTGAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy 1201  TGTGCAGCCCATCCGCTCCACAGAGAGTCTCCCACTCTAGACTTCTGCATCACGATGT 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201  TGTGCAGCCCATCCGCTCCACAGAGAGTCTCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy 1261  TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTTGTCTTCAACCTACCTGTATGCTCTAC 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261  TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTTGTCTTCAACCTACCTGTATGCTCTAC 1320

Qy 1321  ACCTGAGCTCACTGCACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321  ACCTGAGCTCACTGCACCTCTGCCTCCCAGGTTCAAGCAATTCTCCCTGTCTCAGCCTCC 1380

Qy 1381  CCGGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTGTATTGTTAGTAGAGATGGG 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381  CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTGTATTGTTAGTAGAGATGGG 1440

Qy 1441  GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1441  GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy 1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCTAAACACAGGGAAACAGACAAAGCTGTGT 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCTAAACACAGGGAAACAGACAAAGCTGTGT 1560

Qy 1561  TTAATAAGGAATAACTTGAATGTTTACTAAACCAACAGGGAAACAGACAAAGCTGTGA 1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1561  TTAATAAGGAATAACTTGAATGTTTACTAAACCAACAGGGAAACAGACAAAGCTGTGA 1620

Qy 1621  TAATTTCAGGGATTCTTGGGATTGGGATGGGATGAGCTGCCTAGTCCCAGAC 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1621  TAATTTCAGGGATTCTTGGGATTGGGATGGGATGAGCTGCCTAGTCCCAGAC 1680

Qy 1681  CACTGGTCCTCCATCACTTCTCCCTCATCCTTCAGGCTAAGTTACCATTTTATT 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1681  CACTGGTCCTCCATCACTTCTCCCTCATCCTTCAGGCTAAGTTACCATTTTATT 1740

Qy 1741  CACCATGCTTTTGTGTTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1741  CACCATGCTTTTGTGTTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy 1801  TTCCATTTGGGGCCATCTGTGTGTATAGGGGAGGGGCATACCCCAGAGACTCCT 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1801  TTCCATTTGGGGCCATCTGTGTGTATAGGGGAGGGGCATACCCCAGAGACTCCT 1860

Qy 1861  TGAAGCCCCCGGCAGAGGTTTCCTGCAGCCCGTGCCACTCGTTGTTTTATCATTCATTGGACACTGC 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1861  TGAAGCCCCCGGCAGAGGTTTCCTGCAGCCCGTGCCACTCGTTGTTTTATCATTCATTGGACACTGC 1920

Qy 1921  TGGGTGTCCTGAGCAACCTGCCAGCCCTCGGTGTTGTTTTGTTATCACTTCCTAGG 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1921  TGGGTGTCCTGAGCAACCTGCCAGCCCTCGGTGTTGTTTTGTTATCACTTCCTAGG 1980

Qy 1981  GACCTGTTGCTTTCTATTTCTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1981  GACCTGTTGCTTTCTATTTCTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy 2041  TATTGAGTACTTATATCGTCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2041  TATTGAGTACTTATATCGTCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy 2101  CCTACCTTCGTGGAGTGACAGTTTCTCATGGAGAAGACTGCGAAGAAATTAATAGCCA 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2101  CCTACCTTCGTGGAGTGACAGTTTCTCATGGAGAAGACTGCGAAGAAATTAATAGCCA 2160

Qy 2161  GCCAACTTAAACCCAGTCCAGTGCTGAAAGAAAGGAAGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db 2161  GCCAACTTAAACCCAGTCCAGTGCTGAAAGAAAGGAAGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
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Db  2161 GCCAACTTAAACCCAGTGCTGAAAGAAGAAATAAACACCATGCTGCCTCGTGCCGGGAGG 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2221 AGCATCCCTTAACAAGGCCACCTCCCTAGGCGCCCCCTGCTGCCTCCATCGTGCCGGGAGG 2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 AGCATCCCTTAACAAGGCCACCTCCCTAGGCGCCCCCTGCTGCCTCCATCGTGCCGGGAGG 2280

Qy  2281 CCCCAAGCCCGAGTCTTCCAAGCCTCCTCTCCATCAGTCACAGCGCGTCGAGCTGGCCT 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 CCCCAAGCCCGAGTCTTCCAAGCCTCCTCTCCATCAGTCACAGCGCGTCGAGCTGGCCT 2340

Qy  2341 GCCTCGCTTCCCGTGAATGTCTCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 GCCTCGCTTCCCGTGAATGTCTCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy  2401 CCAGAAAGGAAATGGAGAGGAGGGGAACTAGTCTAACGGAGAATCTGAGGGGACAGTGTTTC 2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 CCAGAAAGGAAATGGAGAGGAGGGGAACTAGTCTAACGGAGAATCTGAGGGGACAGTGTTTC 2460

Qy  2461 CTCAGAGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCGAGGGAG 2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CTCAGAGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCGAGGGAG 2520

Qy  2521 TGGGGACGCGTCGGGGCGTGAGCGGGGTCGTGAGGGCTGAAAAGGGCAAGGCTGAA 2580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 TGGGGACGCGTCGGGGCGTGAGCGGGGTCGTGAGGGCTGAAAAGGGCAAGGCTGAA 2580

Qy  2581 GCTGCCCAGATGTGTTCAGTGTGTTCACGGGCGTCGGGAGTTTTCCGTTCCTGTGAGC 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 GCTGCCCAGATGTGTTCAGTGTGTTCACGGGCGTCGGGAGTTTTCCGTTCCTGTGAGC 2640

Qy  2641 CTTTTTATCTTTCTTCTGCTTGGAGGAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 CTTTTTATCTTTCTTCTGCTTGGAGGAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy  2701 ATAAAGTCAGCTGTTAAAATTCAGGGGTGTGCATGGGTTTCTTCACGGAAGGCCTTTAT 2760
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 ATAAAGTCAGCTGTTAAAATTCAGGGGTGTGCATGGGTTTCTTCACGGAAGGCCTTTAT 2760

Qy  2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCGTTAATTCACGGAAGAAGTGAC 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCGTTAATTCACGGAAGAAGTGAC 2820

Qy  2821 TGGAGTCTTTTCTTCATGTCTTCTGGGCAACTACTCCAGCCCTGGTTGGGACTTGGCTTA 2880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 TGGAGTCTTTTCTTCATGTCTTCTGGGCAACTACTCCAGCCCTGGTTGGGACTTGGCTTA 2880

Qy  2881 TGCCAAGACGGTCGAAAAACCTTGGAAATCAGGAGACTCGGTTTCTTCTTCGGTTCTCGCATT 2940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 TGCAAGACGGTCGAAAAACCTTGGAAATCAGGAGACTCGGTTTCTTCTTCGGTTCTCGCATT 2940

Qy  2941 GGTTGGCTGTGCGACCGTGGGCAAGTGCTGTCTCTCCTTCCTTCGGGCCCATAGTCTTCTCTGCT 3000
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 GGTTGGCTGTGCGACCGTGGGCAAGTGCTGTCTCTCCTTCCTTCGGGCCCATAGTCTTCTCTGCT 3000

Qy  3001 ATAAAGACCCTTGCAGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 ATAAAGACCCTTGCAGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3060

Qy  3061 GGATGTTGAGAGGGAACGGGAGGAGCTGAGCGACTGGAGCAGAGGGGAGGTGGAGGGG 3120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 GGATGTTGAGAGGGAACGGGAGGAGCTGAGCGACTGGAGCAGAGGGGAGGTGGAGGGG 3120

Qy  3121 GGACAGGAAGGCAGCAGCAGGGAGGACGCGGGTGCTCCATCAGTCGTCCATCACGTCAGACTC 3180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 GGACAGGAAGGCAGCAGCAGGGAGGACGCGGGTGCTCCATCAGTCGTCCATCACGTCAGACTC 3180

Qy  3181 CAGGACCCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTTCCT 3240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 CAGGACCCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTTCCT 3240

Qy  3241 TCCCTAAGCATAGACAATGGCATTGCCAATAACCAAAAAGAATGCGAGAGACTAACTGGT 3300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 TCCCTAAGCATAGACAATGGCATTGCCAATAACCAAAAAGAATGCGAGAGACTAACTGGT 3300
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Qy  3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGCAAGCAAGTGGAAAATGCCAGAGATTG 3360
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Db  3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGCAAGCAAGTGGAAAATGCCAGAGATTG 3360

Qy  3361 TTAAACTTTTCACCCTGACACAGCACCCAGCAGTCAGCGTCTGACAGCACGG 3420
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 TTAAACTTTTCACCCTGACACAGCACCCAGCAGTCAGCGTCTGACAGCACGG 3420

Qy  3421 AGTGACCTGCAGCGCAGCGGGGAGGAGAAAAGAGGAGTAGTGTATGAGCAAGAAAG 3480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 AGTGACCTGCAGCGCAGCGGGGAGGAGAAAAGAGGAGTAGTGTATGAGCAAGAAAG 3480

Qy  3481 ACAGATTCATTCAAGGCAGTGGGAATTGACCACCAGGGATTATAGTCCACGTGATCCTGG 3540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 ACAGATTCATTCAAGGCAGTGGGAATTGACCACCAGGGATTATAGTCCACGTGATCCTGG 3540

Qy  3541 GTTCTAGGAGGCAGGCTATATTGTGGGGGAAAAAATCAGTTCAAGGGAGTCGGGAGA 3600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 GTTCTAGGAGGCAGGCTATATGTGGGGGAAAAAATCAGTTCAAGGGAGTCGGGAGA 3600

Qy  3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660

Qy  3661 GTAGTAACTGAGGCTGTAAGATAACTTAGTTCTCCTTATTAGAGAACTCTTTTTCTCTGT 3720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GTAGTAACTGAGGCTGTAAGATAACTTAGTTCTCCTTATTAGAGAACTCTTTTTCTCTGT 3720

Qy  3721 GGAGTTAGCACAAAGGGCAATCCCGTTTCTTTAACAGGAAGAAAACATTCCTAAGAG 3780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 GGAGTTAGCACAAAGGGCAATCCCGTTTCTTTAACAGGAAGAAAACATTCCTAAGAG 3780

Qy  3781 TAAAGCCAAACAGATTCAAGCGTGCATGGGTTTTCACTTATGAATGGTTTTTGAAAAAT 3840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 TAAAGCCAAACAGATTCAAGCGTGCATGGGTTTTCACTTATGAATGGTTTTTGAAAAT 3840

Qy  3841 CATTTCAGCGATGTTACTATCTGATTCAGAAAATGAGACTAGTAGACTACCCTTGGTCAGCTG 3900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 CATTTCAGCGATGTTACTATCTGATTCAGAAAATGAGACTAGTAGACTACCCTTGGTCAGCTG 3900

Qy  3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTGGCTTAACTGCAGAACCAATCAAA- 3959
         ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db  3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTGGCTTAACTGCAGAACCAATCAAAT 3960

Qy  3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019
         ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db  3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019

Qy  4020 CAGTTTGAAATATTTACTTCACAAGTATTGGATTGTTGGTATTAACAACATAAAG 4079
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4020 CAGTTTGAAATATTTACTTCACAAGTATTGGATTGTTGGTATTAACAACATAAAG 4079

Qy  4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139

Qy  4140 TTTATTGGCTATTGCCATTTGTTTTTGTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4140 TTTATTGGCTATTGCCATTTGTTTTTGTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199

Qy  4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAATTACATTT 4259
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAATTACGTTT 4259

Qy  4260 TTGTTTTTACCACCTTCTAACTAAATTTATTCCATTGCGAATAGAGCCATAA 4319
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4260 TTATTTTTACCACCTTCTAACTAAATTTATTCCATTGCGAATAGAGCCATAA 4319

Qy  4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
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;  FILE REFERENCE: 07425.0057.US01
;  CURRENT APPLICATION NUMBER: US/10/244,633
;  CURRENT FILING DATE: 2002-09-17
;  PRIOR APPLICATION NUMBER: US/09/306,828
;  PRIOR FILING DATE: 1999-05-07
;  PRIOR APPLICATION NUMBER: US 09/227,881
;  PRIOR FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: Microsoft Word 97
;  SEQ ID NO 2
;  LENGTH: 5304
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-244-633-2

Query Match         99.1%;   Score 5224.4;  DB 43;  Length 5304;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 5264;  Conservative   0;  Mismatches  6;  Indels  6;  Gaps  3;

Qy     1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy    61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAGATCA 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAGATCA 120

Qy   121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCGTGTCTGCTGTTCTTATTTTAGTGA 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCGTGTCTGCTGTTCTTATTTTAGTGA 180

Qy   181 CAGATGTGCTCCTGACAGAGAACTATTCTTCAGGAACATCACATCCAATGGTAAATC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CAGATGTGCTCCTGACAGAGAACTATTCTTCAGGAACATCACATCCAATGGTAAATC 240

Qy   241 CATCAACACAGAGAGTAAGAAACAGGAAACAGGAATGAGATGGGGCACTTGCCCAAGGAAAAATGCCAG 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CATCAACACAGAGAGTAAGAAACAGGAAACAGGAATGAGATGGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy   301 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTAATTTCAGGAAAAAATG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTAATTTCAGGAAAAAATG 360

Qy   361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAGATGTTTCCAAATTGG 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAGATGTTTCCAAATTGG 420

Qy   421 TAATTAAGTAATTGTTCCTTGGGAAGACCTCCATGTGAGCTGATGGGAAATGGGAA 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TAATTAAGTAATTGTTCCTTGGGAAGACCTCCATGTGAGCTGATGGGAAATGGGAA 480

Qy   481 AAACGTCAAAAGCATGCATGTTCAGGAGGTCATGTTAGCAAAGGACATAACAATAAC 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AAACGTCAAAAGCATGCATGTTCAGGAGGTCATGTTAGCAAAGGACATAACAATAAC 540

Qy   541 GGCATCACTCTGGGAGGCAAGTCAAATGCAGGAGGAAAATGGGGACTCGGGCAGCAAGG 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGCATCACTCTGGGAGGCAAGTCAAATGCAGGAGGAAAATGGGGACTCGGGCAGCAAGG 600

Qy   601 AGCAAAATCAAAATTCCGACAAATGCAAAATCAAAATTCCGACAAATGAGCCAAGCTTTCATAAC 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AGCAAAATCAAAATTCCGACAAATGCAAAATCAAAATTCCGACAAATGAGCCAAGCTTTCATAAC 660

Qy   661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCATACCAGGAACACAAAA 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCATACCAGGAACACAAAA 720

Qy   721 ATTGACTGGGCTAAGCCTGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAA 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATTGACTGGGCTAAGCCTGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAA 780

Qy   781 GACATGTGTTAAAAGGAACCAGAACATTGTGAGCCTTCAAGCAGCAGTGCCCCTCAGCA 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||


Qy  4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439

Qy  4440 ACTTTGAAATTAGACCTTCCTGCTGGATCTTGTTTTTAACATATTAATAATAAAACATGTTTAA 4499
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4440 ACTTTGAAATTAGACCTTCCTGCTGGATCTTGTTTTTAACATATTAATAATAAAACATGTTTAA 4499

Qy  4500 AATTTTGATATTTGATAATCATATTCATTATCATTTGTTTCCTTGTAATCTATATTT 4559
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4500 AATTTTGATATTTGATAATCATATTCATTATCATTTGTTTCCTTGTAATCTATATTT 4559

Qy  4560 TATATATTTGAAAAACATCTTTCTGAGAAGAGTCCCAGATTTCACCAATGAGGTTCTTG 4619
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4560 TATATATTTGAAAAACATCTTTCTGAGAAGAGTCCCAGATTTCACCAATGAGGTTCTTG 4619

Qy  4620 GCATGCACACACAGAGTAAGAACTGATTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4620 GCATGCACACACAGAGTAAGAACTGATTAGAGGCTAACATTGACATTGGTGCCTGAG 4679

Qy  4680 ATGCAAGACTGAAATTAGAAGTTCTTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4680 ATGCAAGACTGAAATTAGAAGTTCTTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739

Qy  4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799

Qy  4800 CCTTGTGTTCTGGCTGTGTATTTTCTCTGTCCCGTCTTAAAGGACTTGTT 4859
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4800 CCTTGTGTTCTGGCTGTGTATTTTCTCTGTCCCGTCTTAAAGGACTTGTT 4859

Qy  4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTTCTCAATGAGTTTGCAGA 4919
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTTCTCAATGAGTTTGCAGA 4919

Qy  4920 GTGAATGGAAATAATAAACTAGAAATATATCCTTGTTGAAATCAGCACCAGTAGTCCTG 4979
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4920 GTGAATGGAAATAATAAACTAGAAATATATCCTTGTTGAAATCAGCACCAGTAGTCCTG 4979

Qy  4980 GTGTAAGTGTGTAC---GTGTGTGTGTGTGTGTGTGTGTGTAAACCAGGTGG 5035
           ||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db  4980 GTGTAAGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAACCAGGTGG 5039

Qy  5036 AGATATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTAAAAAGA 5095
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5040 AGATATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTAAAAAGA 5099

Qy  5096 AACTCCAAACAGACTTCTGGAAGGTTATTTCTAAGAATCTTGCTGCGGCGTGAAGGCA 5155
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5100 AACTCCAAACAGACTTCTGGAAGGTTATTTCTAAGAATCTTGCTGCGGCGTGAAGGCA 5159

Qy  5156 ACCCCCTGTGCACAGCCCCACCACCCCACCGCTCACGTGGCCACCTCTCGTCTTCCTGTCTT 5215
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5160 ACCCCCTGTGCACAGCCCCACCACCCCACCGCTCACGTGGCCACCTCTCGTCTTCCTGTCTT 5219

Qy  5216 GGCTGGCTCCCCAGTATATATAAACCTCTCTGAGCTCGGGCATGAGCCAGCAAGG 5271
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5220 GGCTGGCTCCCCAGTATATATAAACCTCTCTGAGCTCGGGCATGAGCCAGCAAGG 5275
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RESULT 14
US-10-244-633-2
; Sequence 2, Application US/10244633
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
; TITLE OF INVENTION: Disorders

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Db   781  GACATGGTTAAAAGGCAACCAGAACATTGTCAGCCTTCAAAGCAGCAGTGCCCCTCAGCA  840

Qy   841  GGGACCCTGAGGCATTGCCTTGCCCTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  GGGACCCTGAGGCATTGCCCTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC  900

Qy   901  TTGAAAGATCATGAATTTTAACCATTTTAGTAGTATAAAACAAATATGCATGCATAAATCAG  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  TTGAAAGATCATGAATTTTAACCATTTTAGTAGTATAAAACAAATATGCATGCATAAATCAG  960

Qy   961  TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC  1020

Qy  1021  GGATAGGTCAGAAATCATTAGAAATCACTGTCCCCATCCTAACTTTTTCAGAATGATC  1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGATAGGTCAGAAATCATTAGAAATCACTGTCCCCATCCTAACTTTTTCAGAATGATC  1080

Qy  1081  TGTCATAGCCCTCACACAGCGCCCGATGTGCTGACCTACAACCACATCTACAACCCAA  1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  TGTCATAGCCCTCACACAGCGCCCGATGTGCTGACCTACAACCACATCTACAACCCAA  1140

Qy  1141  GTGCCTCAACCATTGTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GTGCCTCAACCATTGTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC  1200

Qy  1201  TGTGCAGCCCATCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT  1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  TGTGCAGCCCATCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT  1260

Qy  1261  TACAGCCCAGAAGCTCCGTGAGGGTGAGGGTGAGGGTCTGTTCTTACACCTACCTGTATGCTCTAC  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  TACAGCCCAGAAGCTCCGTGAGGGTGAGGGTGAGGGTCTGTTCTTACACCTACCTGTATGCTCTAC  1320

Qy  1321  ACCTGAGCTCACTGCAACCTCTGCCTCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC  1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  ACCTGAGCTCACTGCAACCTCTGCCTCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC  1380

Qy  1381  CGCGTAGCTGGGACTACAGGCGCGACGCCGCCACGCCCCGGCGTAATTTTGTATTGTTAGTAGAGATGGG  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CGCGTAGCTGGGACTACAGGCGCGACGCCGCCACGCCCCGGCGTAATTTTGTATTGTTAGTAGAGATGGG  1440

Qy  1441  GTTTCACCCATATTAGCCCGGCTCGGTCTTGAACTCCTGACCTCAGGTGATCTCACCCACCTC  1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  GTTTCACCCATATTAGCCCGGCTCGGTCTTGAACTCCTGACCTCAGGTGATCTCACCCACCTC  1500

Qy  1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCCGCCCGGCCAAGGGTCAGTGT  1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCCGCCCGGCCAAGGGTCAGTGT  1560

Qy  1561  TTAATAAGGAATAACTTGAATGGTTACTAAACCAACAGAGGGAAACAGACAAAAGCTGTGA  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  TTAATAAGGAATAACTTGAATGGTTACTAAACCAACAGAGGGAAACAGACAAAAGCTGTGA  1620

Qy  1621  TAATTTCAGGGATTCTTCGGGATGGGGAATGGTCCATGAGCTGCCTGCCTAGTCCCCAGAC  1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  TAATTTCAGGGATTCTTCGGGATGGGGAATGGTCCATGAGCTGCCTGCCTAGTCCCCAGAC  1680

Qy  1681  CACTGGTCCTCATCACTTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT  1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  CACTGGTCCTCATCACTTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT  1740

Qy  1741  CACCATGCTTTTGTGGTAAGCCTTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG  1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  CACCATGCTTTTGTGGTAAGCCTTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG  1800

Qy  1801  TTCCATTTGGGGCCATCGTGTGTGTGTGTATAGGGGAGGAGGGCCATACCCCAGAGACTCCT  1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  TTCCATTTGGGGCCATCGTGTGTGTGTGTATAGGGGAGGAGGGCCATACCCCAGAGACTCCT  1860

Qy  1861  TGAAGCCCCCGCGCAGAGTTTCCTCTCCAGCTGGGGAGCCCTGCAAGCACCCGGGGTCC  1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  TGAAGCCCCCGCGCAGAGTTTCCTCTCCAGCTGGGGAGCCCTGCAAGCACCCGGGGTCC  1920
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Qy  1921  TGGGGTGTCCTGAGCAACCTGCCGCCACTGGTTGTTTGTTATCACTCTCTAGG  1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  TGGGGTGTCCTGAGCAACCTGCCGCCACTGGTTGTTTGTTATCACTCTCTAGG  1980

Qy  1981  GACCTGTTGCTTCTTCATTCGTGTGACTCGTTCATTCATTCATTGACAATT  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  GACCTGTTGCTTCTTCATTCGTGTGACTCGTTCATTCATTCATTGACAATT  2040

Qy  2041  TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGTGAGCAAGCAGTCACTGC  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGTGAGCAAGCAGTCACTGC  2100

Qy  2101  CCTACCTTCGTGGAGTGACAGTTTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA  2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCTACCTTCGTGGAGTGACAGTTTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA  2160

Qy  2161  GCCAACTTAAACCCAGTGTGTGAAAGAAATAAACCACCATCTTGAAGAATTGTGCGC  2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GCCAACTTAAACCCAGTGTGTGAAAGAAATAAACCACCATCTTGAAGAATTGTGCGC  2220

Qy  2221  AGATCCCTTAACAGAGCCACCTCCTCCTCCAAGCGTGCCTCCATCGTGTGCCCGAGG  2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  AGATCCCTTAACAGAGCCACCTCCTCCTCCAAGCGTGCCTCCATCGTGTGCCCGAGG  2280

Qy  2281  CCCCCAAGCCCGAGTCTTCCAAGCTCTCCTCCTCCATCAGTCACAGGGCTGCGAGCTGCCT  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  CCCCCAAGCCCGAGTCTTCCAAGCTCTCCTCCTCCATCAGTCACAGGGCTGCGAGCTGCCT  2340

Qy  2341  GCCTCGCTTCCCGTGAATCGTCCTGGTCATCTGAGCTGCTGAGCTGGAGACTCCTTGGCTCCAGGCT  2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  GCCTCGCTTCCCGTGAATCGTCCTGGTCATCTGAGCTGCTGAGCTGGAGACTCCTTGGCTCCAGGCT  2400

Qy  2401  CCAGAAAGGAAATGGAGAGGAAACTAGTCTAACGGAGAATCTGAGGAGGTGGGGACTGCAGGGAG  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  CCAGAAAGGAAATGGAGAGGAAACTAGTCTAACGGAGAATCTGAGGAGGTGGGGACTGCAGGGAG  2460

Qy  2461  CTCAGAGGGAAAAGGGCCTTCCACGTCCACGTCCAGGAGGTGCTGAAAAGGCAGGAGGCTGAA  2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  CTCAGAGGGAAAAGGGCCTTCCACGTCCACGTCCAGGAGGTGCTGAAAAGGCAGGAGGCTGAA  2520

Qy  2521  TGGGGACGCTGGGCTGGGCTGAGCGGGTGCTGAAAGGCAGGAGGTGAAAAGGGCAAGGCTGAA  2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  TGGGGACGCTGGGCTGGGCTGAGCGGGTGCTGAAAGGCAGGAGGTGAAAAGGGCAAGGCTGAA  2580

Qy  2581  GCTGCCCAGATGTTCAGTGTGTTCAGTGTGTTCTGGAGTTTCCGTTGCTTCCTGTGAGC  2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  GCTGCCCAGATGTTCAGTGTGTTCAGTGTGTTCTGGAGTTTCCGTTGCTTCCTGTGAGC  2640

Qy  2641  CTTTTATCTTTTCTCTGCTTGGAGGAGGAGAGTCTATTTCATGAAGGGATGCAGTTTTC  2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  CTTTTATCTTTTCTCTGCTTGGAGGAGGAGAGTCTATTTCATGAAGGGATGCAGTTTTC  2700

Qy  2701  ATAAAGTCAGCTGTTAAAATTCAGGTGTGCATGGGTTTCCTTCACGAGGCCTTTAT  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  ATAAAGTCAGCTGTTAAAATTCAGGTGTGCATGGGTTTCCTTCACGAGGCCTTTAT  2760

Qy  2761  TTAATGGAATATAGGAAGCGAGCTCATTTCCTGGCTAAGTTACCATTTTATTCACGGAAGTGAC  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  TTAATGGAATATAGGAAGCGAGCTCATTTCCTGGCTAAGTTACCATTTTATTCACGGAAGTGAC  2820

Qy  2821  TGGAGTCTTTTCTTTCATGTCTTCTCGGGCAACTACTCAGCCCGTGGTTGGACTTGGCTTA  2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  TGGAGTCTTTTCTTTCATGTCTTCTCGGGCAACTACTCAGCCCGTGGTTGGACTTGGCTTA  2880

Qy  2881  TGCAAGACGGTCGAAAACCTTGCAAACCTTGAATCAGGAGACTCGGTTTTCTTCGGTTCTGCCATT  2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  TGCAAGACGGTCGAAAACCTTGCAAACCTTGAATCAGGAGACTCGGTTTTCTTCGGTTCGCCATT  2940

Qy  2941  GGTTGGCTGTGCGACCTGGGCAAGTGTCTCTCTTCCTTCCCTCCGGGCCATAGTCTTTCTGCT  3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  GGTTGGCTGTGCGACCTGGGCAAGTGTCTCTCTTCCTTCCCTCCGGGCCATAGTCTTCTCTGCT  3000
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Db   5160 ACCCCCCTGTGCACAGCCCACCCAGCCTCACGTGGCCACCTCTGTCTCCCCATGAAG 5219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5216 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5220 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5275
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RESULT 15
US-60-172-360-23886
; Sequence 23886, Application US/60172360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymorp
; FILE REFERENCE: GX-0007 P
; CURRENT APPLICATION NUMBER: US/60/172,360
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 29838
; SOFTWARE: PERL Program
; SEQ ID NO 23886
; LENGTH: 7369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 223079.1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1321-1562, 4158-4182, 4874-4912, 4986-5023
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-360-23886

Query Match   93.4%; Score 4925.4; DB 75; Length 7369;
Best Local Similarity   93.5%; Pred. No. 0;
Matches 4926; Conservative   0; Mismatches   345; Indels   0; Gaps   0;

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Qy      1 ATCTTTGTTCAGTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db      1 ATCTTTGTTCAGTTACCTCAGGGCTATTATGAAATGAAATGAAATGAACCAATGTGAAAG 60

Qy     61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy    121 GGAAGAAGGAGGTATCCACGTTAGCCAAGTGTCCAAGTGTCCAGG 180
          |||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGAAGAAGGAGGTATCCACGTTAGCCAAGTGTCCAAGTGTCCAGG 180

Qy    181 CAGATGTTGCTCCTGACGAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CAGATGTTGCTCCTGACGAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy    241 CATCAAACAGGAGCTAAGAAACAGGAATGAGAATGAGATGGGCACTTGCCCAGGAAAATGCCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CATCAAACAGGAGCTAAGAAACAGGAATGAGAATGAGATGGGCACTTGCCCAGGAAAATGCCAG 300

Qy    301 GAGAGCAAATAATGATGAGAAAATAAACTTTCCCTTTGTTTTTAATTTCAGGAGAAAAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAGAGCAAATAATGATGAGAAAATAAACTTTCCCTTTGTTTTTAATTTCAGGAGAAAAAATG 360

Qy    361 ATGAGGACCAAAATCAATGATAAGGAAAAACAGCTCAGAAAAAGATGTTTCCAAATTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATGAGGACCAAAATCAATGATAAGGAAAAACAGCTCAGAAAAAGATGTTTCCAAATTGG 420

Qy    421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTTCCATGTGAGCTTGATGGAAAATGGGAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTTCCATGTGAGCTTGATGGGAAATGGGAA 480

Qy    481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAACCAGAT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAACCAGAT 540

Qy    541 GGCATCACTCTGGGAGGCAAGTTCAGGAGGTCATGTTAGCAAAGGACATAACAATAAC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGCATCACTCTGGGAGGCAAGTTCAGGAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy    601 AGCAAAATCAAAATTCCGCAACTTCCGCAAATGAGAGGAGAGAAATGGGGACTGGGAAAGCTTCATAAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCAAAATCAAAATTCCGCAACTTCCGCAAATGAGAGGAGAGAAATGGGGACTGGGAAAGCTTCATAAC 660

Qy    661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy    721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGACGAAAAACAAAA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGACGAAAAACAAAA 780

Qy    781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy    841 GGGACCCTGAGGCATTGCCTTAGGAAGGCCAGTTTTCTTAAGGAAATCTTAAGAAACTC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGGACCCTGAGGCATTGCCTTAGGAAGGCCAGTTTTCTTAAGGAAATCTTAAGAAACTC 900

Qy    901 TTGAAAGATCATGAATTTAACCATTTAAGTATAAAAACAAAATATGCGATGCATAATCAG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TTGAAAGATCATGAATTTAACCATTTAAGTATAAAAACAAAATATGCGATGCATAATCAG 960

Qy    961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy   1021 GGATAGGTCAGAAATCATTAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTTCAGAATGATC 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGATAGGTCAGAAATCATTAGAAATCATTAGAAATCACTGTGTCCCATCCTAACTTTTTCAGAATGATC 1080

Qy   1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACACCACATCTACAACCCAA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACACCACATCTACAACCCAA 1140

Qy   1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy   1201 TGTGCAGCCCATCCCGCTCCCACAGGAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TGTGCAGCCCATCCCGCTCCCACAGGAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy   1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCGTGTCTTGTGTCTTGTGTCTTACCTCTAC 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCGTGTCTTGTGTCTTGTGTCTTACCTCTAC 1320

Qy   1321 ACCTGAGCTCACTGCAACCTCTGCTCCCCCAGGTTCAAGCAGTTCAGCAATTCTCTGTCTCTCAGCCTC 1380
          NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Db   1321 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1380

Qy   1381 CCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGG 1440
          NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Db   1381 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1440

Qy   1441 GTTTCACCCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCACCTC 1500
          NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Db   1441 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1500

Qy   1501 AGCCTCCTAAAGTGCTGGGATTACAGGCGCATGAGACTCACCCGGCCCGGCCCAAGGGTCAGTGT 1560
          NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Db   1501 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1560

Qy   1561 TTAATAAGGAATAACTTGAATCGTTTACTAAACCAACAGGGAAACAGACAAACAGACAAAAGCTGTGA 1620
          NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Db   1561 NNAATAAGGAATAACTTGAATCGTTTACTAAACCAACAGGGAAACAGACAAACAGACAAAAGCTGTGA 1620
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Qy  1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTAGTCCCAGAC 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTAGTCCCAGAC 1680

Qy  1681 CACTCGTCCTCATCACTTTCTTCCTCATCCTCATTTCAGGCTAAGTTACCATTTATT 1740
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Db  1681 CACTCGTCCTCATCACTTTCTTCCTCATCCTCATTTCAGGCTAAGTTACCATTTATT 1740

Qy  1741 CACCATGCTTTGTGTGAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 CACCATGCTTTGTGTGAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy  1801 TTCCATTTGGGGCCATCTGTGTGTGTATAGGGAGGAGGCATACCCCAGAGACTCCT 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 TTCCATTTGGGGCCATCTGTGTGTGTATAGGGAGGAGGCATACCCCAGAGACTCCT 1860

Qy  1861 TGAAGCCCCGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCCTGCAAGCACCCGGGGTCC 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 TGAAGCCCCGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCCTGCAAGCACCCGGGGTCC 1920

Qy  1921 TGGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTCGGTTGTTTTGTTATCACTCTCTAGG 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 TGGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTCGGTTGTTTTGTTATCACTCTCTAGG 1980

Qy  1981 GACCTGTGCTTCTATTTCTGTGTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 GACCTGTGCTTCTATTTCTGTGTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy  2041 TATTGAGTACTTATATCTGCCAGAACCAGACAAAATGTGAGCAAAGCAGTCACTGC 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 TATTGAGTACTTATATCTGCCAGAACCAGACAAAATGTGAGCAAAGCAGTCACTGC 2100

Qy  2101 CCTACCTTCGTTGGAGGTGACAGTTTCTCATGGAGACGTGCAGAGAAAATTAATAGCCA 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 CCTACCTTCGTTGGAGGTGACAGTTTCTCATGGAGACGTGCAGAGAAAATTAATAGCCA 2160

Qy  2161 GCCAACTTAAACCCAGTCGTGCTGAAAGAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCCAACTTAAACCCAGTCGTGCTGAAAGAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy  2221 AGCATCCCTTAACAAGGCCACCTCCTCCCTAGCCCTGTGCTCCATCGTGCCCGGAGG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 AGCATCCCTTAACAAGGCCACCTCCTCCCTAGCCCTGTGCTCCATCGTGCCCGGGGG 2280

Qy  2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCATCGACAGCCGCTGCAGCTGGCTCT 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCATCGACAGCCGCTGCAGCTGGCTCT 2340

Qy  2341 GCCTCGCTTCCCTGAATCGTCCGTGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 GCCTCGCTTCCCTGAATCGTCCGTGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy  2401 CCAGAAAGGAAATGAGAGGAGAAACTAGTCTAACGGAAGAATTCCAGGAAGGTGAA 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 CCAGAAAGGAAATGAGAGGAGAAACTAGTCTAACGGAAGAATTCCAGGAAGGTGAA 2460

Qy  2461 CTCAGAGGGAAAGGGGGCCTCCACGTCGGGGCGGGGCTGAGCGGGTGGGGACTGGGACTGTTTC 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CTCAGAGGGAAAGGGGGCCTCCACGTCGGGGCGGGGCTGAGCGGGTGGGGACTGGGACTGTTTC 2520

Qy  2521 TGGGGACGCTGGGGGCTGAGCGGGCTGAGCGGGCTGAGCGGGTGAAAAGGCAAGGCTGAA 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 TGGGGACGCTGGGGGCTGAGCGGGCTGAGCGGGCTGAGCGGGTGAAAAGGCAAGGCTGAA 2580

Qy  2581 GCTGCCCAGATGTTCAGTGTTGTCACGGGGCTGGGAGTTTCCGTTGCTTCTCCGTGAGC 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 GCTGCCCAGATGTTCAGTGTTGTCACGGGGCTGGGAGTTTCCGTTGCTTCTCCGTGAGC 2640

Qy  2641 CTTTTATCTTTTCTCTGCTTGGAGGAAGAAGAGTCTATTCATGAAGGGATGCAGTTTC 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 CTTTTATCTTTTCTCTGCTTGGAGGAAGAAGAGTCTATTCATGAAGGGATGCAGTTTC 2700

Qy  2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGGAAGGCCTTTAT 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGGAAGGCCTTTAT 2760

Qy  2761 TTAATGGAATATAGGAAGCGAGCTCATTTCCGTTAATTCACGGAAGAAGTGAC 2820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 TTAATGGAATATAGGAAGCGAGCTCATTTCCGTTAATTCACGGAAGAAGTGAC 2820

Qy  2821 TGGAGTCTTTTCTTTCATGTCTTTCTGGGCAACTACTCAGCCCGTGTGGGACTTGGCTTA 2880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 TGGAGTCTTTTCTTTCATGTCTTTCTGGGCAACTACTCAGCCCGTGTGGGACTTGGCTTA 2880

Qy  2881 TGCAAGACGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCGGTTCTGCCATT 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 TGCAAGACGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCGGTTCTGCCATT 2940

Qy  2941 GGTTGGCTGTGCGACCGTGCAAGTGTCTCTCCTTCCTTCCCTGGGCCATAGTCTTCTGCT 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 GGTTGGCTGTGCGACCGTGCAAGTGTCTCTCCTTCCTTCCCTGGGCCATAGTCTTCTGCT 3000

Qy  3001 ATAAAGACCCTTGCAGCTCTCGAGTTCTGTGGCACTCCCTGTGAACACTTCCCTGTGTGAGGGG 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 ATAAAGACCCTTGCAGCTCTCGAGTTCTGTGGCACTCCCTGTGAACACTTCCCTGTGTGAGGGG 3060

Qy  3061 GGATGTTGAGAGGGAAGGCAGGCGAGAAGTCGGTGCTCCATCAGTCCTCACTGACTC 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 GGATGTTGAGAGGGAAGGCAGGCGAGAAGTCGGTGCTCCATCAGTCCTCACTGACTC 3120

Qy  3121 GGACAGGAAGCCACCAATGCTTCAGGAAGCTGAGCCAAATGCTTCAGGAAAGTCAATGACACACAATTTCCT 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 GGACAGGAAGCCACCAATGCTTCAGGAAGCTGAGCCAAATGCTTCAGGAAAGTCAATGACACACAATTTCCT 3180

Qy  3181 CAGGACCGAGAGCCAGAGTTCTCAGGAAAGCTTCAGGAAAGCCACATTTCCT 3240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 CAGGACCGAGAGCCAGAGTTCTCAGGAAAGCTTCAGGAAAGCCACATTTCCT 3240

Qy  3241 TCCCTAAGCATAGACAATGCAATTGCCAATAACCAAAAGAATGCAGAGACTAACTGGT 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 TCCCTAAGCATAGACAATGCAATTGCCAATAACCAAAAGAATGCAGAGACTAACTGGT 3300

Qy  3301 GGTAGCTTTGCTGGCATTCAAAAACTGGGCCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 GGTAGCTTTGCTGGCATTCAAAAACTGGGCCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360

Qy  3361 TTAAACTTTCACCCTGACAGCGACTGCTGACAGCACGG 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 TTAAACTTTCACCCTGACAGCGACTGCTGACAGCACGG 3420

Qy  3421 AGTGACCTGCAGCGCCAGGGGAGGAGAAGAAGAGGATAGTGTATGAGCAAGAAAG 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 AGTGACCTGCAGCGCCAGGGGAGGAGAAGAAGAGGATAGTGTATGAGCAAGAAAG 3480

Qy  3481 ACAGATTCATTCAAGGCAGTGGAATTGACCACAGGGAATTGACCACAGGATTATATCAGTCCACGTCATCCTGG 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 ACAGATTCATTCAAGGCAGTGGAATTGACCACAGGGAATTGACCACAGGATTATATCAGTCCACGTCATCCTGG 3540

Qy  3541 GTTCTAGGCAGGCAGGGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 GTTCTAGGCAGGCAGGGGCTATATTGTGGGGGAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600

Qy  3601 CCTGATTTCTAATACTATATTTTCCTTAAGCTGAGTAATTCTGAGCAAGTGGCTCACAAG 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 CCTGATTTCTAATACTATATTTTCCTTAAGCTGAGTAATTCTGAGCAAGTGGCTCACAAG 3660

Qy  3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAAACATTCCTAAGAGCTCTGT 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAAACATTCCTAAGAGCTCTGT 3720

Qy  3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTACCAGGAAGAAAACATTCCTAAGAG 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTACCAGGAAGAAAACATTCCTAAGAG 3780

Qy  3781 TAAAGCCAAACAGATTCAAGCTGTGCATGGGTTTTCCTTCGACTATATGATTGGTTTTTGAAAAT 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 TAAAGCCAAACAGATTCAAGCTGTGCATGGGTTTTCCTTCGACTATATGATTGGTTTTTGAAAAT 3840
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Db  3781 TAAAGCCAAACAGATTCAGCCTAGGTCTTGCTGCTGACTATGATGTTGGTTTTTGAAAAAT 3840

Qy  3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGTCAGCTG 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGTCAGCTG 3900

Qy  3901 TAAACAAACACCCAGTGTAAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901 TAAACAAACACCCAGTGTAAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960

Qy  3961 AGAATAGAATCTTTAGAGGCAAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961 AGAATAGAATCTTTAGAGGCAAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020

Qy  4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
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Db  4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080

Qy  4081 TGCTCAAAGGCAATCATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  4141 TTATTGGCTATTGCCATTTGCTTTTGTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
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Qy  4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
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Qy  4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTATTCCATTGCGAATAGAGCCATAAAA 4320
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Qy  4441 CTTTGAAATTAGACCTCCTCGCTGCTGTGATCTTGTTTTGTCATTAAATAAAAACATGTTTAAA 4500
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Db  4441 CTTTGAAATTAGACCTCCTCGCTGCTGTGATCTTGTTTTGTCATTAAATAAAAACATGTTTAAA 4500

Qy  4501 ATTTTGATATTTTGATAATCATATTTGTTTCCTTTGTAATCTATATTTT 4560
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Db  4501 ATTTTGATATTTTGATAATCATATTTGTTTCCTTTGTAATCTATATTTT 4560

Qy  4561 ATATATTTGAAAACATCTTCTGAGAGAATGCTTCTCCCCAGATTTCACCCAATGAGGTTCTGG 4620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4561 ATATATTTGAAAACATCTTCTGAGAGAATGCTTCTCCCCAGATTTCACCCAATGAGGTTCTGG 4620

Qy  4621 AGGGGGGAAATCTGCCGCTTCTATAGGAAATGCTCTCCCTGGAGCCTTGGTAGGGTGCTGTC 4680
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Qy  5041 TAGGAACTATTATTGGGGTGCATAAATTGGGATGTTCTTTTAAAAAGAAACTC 5100
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Db  5101 CAAACAGACTTCTGGAAGGTATTTTCTAAGAATCTTGCTGGCAGCGGTGAAGGCAACCCCC 5160

Qy  5161 CCTGTGCACAGCCCCACCCAGCCTCAGTGGCCACCTCGTCTTCCCCATGAGACGGGCTG 5220
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Db  5161 CCTGTGCACAGCCCCACCCAGCCTCAGTGGCCACCTCGTCTTCCCCATGAGACGGGCTG 5220

Qy  5221 GCTCCCCAGTATATATAAAACCTCTCTGGAGACTCCGGGCATGAGCCAGCAAGG 5271
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Db  5221 GCTCCCCAGTATATATAAAACCTCTCTGGAGACTCCGGGCATGAGCCAGCAAGG 5271
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Job time : 17364 secs

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: January 26, 2006, 03:03:01 ; Search time 758 Seconds
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Title: US-09-227-881-34
Perfect score: 5271
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Scoring table: IDENTITY_NUC
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Searched: 3416786 seqs, 915751376 residues

Total number of hits satisfying chosen parameters: 6833572

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1		184.8	3.5	1000	11	US-11-266-748A-198985	Sequence 198985
2		184.4	3.5	1000	11	US-11-266-748A-224089	Sequence 224089
3		184.4	3.5	1770	11	US-11-266-748A-26905	Sequence 26905, A
4		184.2	3.5	1000	11	US-11-266-748A-195297	Sequence 195297
5		183.6	3.5	17691	6	US-10-868-184C-6721	Sequence 6721, Ap
6		183.6	3.5	17691	7	US-10-868-184C-6721	Sequence 6721, Ap
7		182.4	3.5	515	11	US-11-266-748A-212844	Sequence 212844, A
8	c	182.4	3.5	515	11	US-11-266-748A-236144	Sequence 236144,
9		180.8	3.4	101500	11	US-11-266-748A-61740	Sequence 61740, A
10		180.6	3.4	39729	11	US-11-214-063A-1285	Sequence 1285, Ap
11		179.4	3.4	10948	11	US-11-214-063A-1715	Sequence 1715, Ap
12	c	179.2	3.4	6708	6	US-10-868-184C-6360	Sequence 6360, Ap
13	c	179.2	3.4	6708	7	US-10-868-184C-6360	Sequence 6360, Ap
14	c	179.2	3.4	6708	6	US-10-868-184C-11267	Sequence 11267, A
15	c	179.2	3.4	6708	7	US-10-868-184C-11267	Sequence 11267, A
16	c	179.2	3.4	189450	1	PCT-US05-10912-6	Sequence 6, Appli
17		179.2	3.4	495475	11	US-11-266-748A-28223	Sequence 28223, A
18	c	178.6	3.4	124048	11	US-11-266-748A-59707	Sequence 59707, A
19	c	177.8	3.4	155379	11	US-11-266-748A-24170	Sequence 24170, A
20	c	177.8	3.4	155379	11	US-11-266-748A-59410	Sequence 59410, A
21		177.8	3.4	227968	11	US-11-266-748A-60135	Sequence 60135, A
22	c	177.6	3.4	128978	11	US-11-266-748A-61436	Sequence 61436, A
23		176.8	3.4	53332	6	US-10-786-065-3	Sequence 3, Appli
24	c	176.8	3.4	53332	7	US-10-786-065-3	Sequence 3, Appli
25	c	176.6	3.4	1173	6	US-10-461-673-4221	Sequence 4221, Ap
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27	c	176	3.3	1400	6	US-10-868-184C-7974	Sequence 7974, Ap
28	c	176	3.3	1400	7	US-10-868-184C-7974	Sequence 7974, Ap
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31		176	3.3	164429	11	US-11-266-748A-22662	Sequence 22662, A
32		175.6	3.3	1000	11	US-11-266-748A-196932	Sequence 196932,
33		175.6	3.3	3143	11	US-11-266-748A-28298	Sequence 28298, A
34		175.4	3.3	6110	11	US-11-266-748A-24483	Sequence 24483, A
35		175.4	3.3	100096	11	US-11-266-748A-59715	Sequence 59715, A
36		175.2	3.3	65854	6	US-10-868-184C-12628	Sequence 12628, A
37	c	175.2	3.3	65854	7	US-10-868-184C-13035	Sequence 13035, A
38		175.2	3.3	65854	7	US-10-868-184C-12628	Sequence 12628, A
39	c	175.2	3.3	65854	6	US-10-868-184C-13035	Sequence 13035, A
40	c	175.2	3.3	822900	11	US-11-214-063A-1393	Sequence 1393, Ap
41		175	3.3	1000	11	US-11-266-748A-197285	Sequence 197285,
42		175	3.3	2297	7	US-10-276-817B-3434	Sequence 3434, Ap
43		175	3.3	2297	6	US-10-276-817B-3434	Sequence 3434, Ap
44	c	175	3.3	6615	11	US-11-266-748A-30008	Sequence 30008, A
45	c	175	3.3	6639	11	US-11-266-748A-30006	Sequence 30006, A

ALIGNMENTS

RESULT 1
US-11-266-748A-198985
; Sequence 198985, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 198985
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-198985

Query Match 3.5%; Score 184.8; DB 11; Length 1000;
Best Local Similarity 78.2%; Pred. No. 5.3e-36;
Matches 222; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 1281 GGGTGAGGGTCTGTGTCTTACACCTGTATGCTCTACACCTGAGCTCACTGCAACCT 1340
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Db 578 GAGTCTCGCTCTGTTACCCATGCTGGAGTGCAGTGGCGCTATCTCAGCTCACTGCAACCT 637

Qy 1553 GTCAGTGTTTAATAAGGAATAACTTGAATGGTTTACTAAACCAA 1596

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RESULT 3
US-11-266-748A-26905/c
; Sequence 26905, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26905
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-26905

Query Match   3.5%; Score 184.4; DB 11; Length 1770;
Best Local Similarity 81.0%; Pred. No. 8.4e-36;
Matches 230; Conservative 0; Mismatches 46; Indels 8; Gaps 1;

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Qy 1381 CGGGTAGCTGGGACTACAGGCG--------CACGCGCCGGCTAATTTTTGTATTGTTAGTA 1432
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Db 1648 CGAGCAGCTGGGACTACAGGCGCCCGACACCACGCCCGGCTAATTTTTGTATTTTTAGTA 1589

Qy 1433 GAGATGGGGTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCA 1492
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Qy 1493 CCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGTCAGGTCACCGGCCCGGCAAGG 1552
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Db 1528 CCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCGATCCGGCCAGAT 1469

Qy 1553 GTCAGTGTTTAATAAGGAATAACTTGAATGGTTTACTAAACCAA 1596
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RESULT 4
US-11-266-748A-195297
; Sequence 195297, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl

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Db   638 CCGCCTCCCGCGGTTCAAGCAATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGG 697

Qy 1401 CGCACGCCCGGCTAATTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCGG 1460
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Db   698 CTCATGCCAATTAATTTTGTATTTTTAGTAGAGTCGGGGTTTCGGTGATGTTGGCCAGG 757

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RESULT 2
US-11-266-748A-224089/c
; Sequence 224089, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 224089
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-224089

Query Match   3.5%; Score 184.4; DB 11; Length 1000;
Best Local Similarity 81.0%; Pred. No. 6.7e-36;
Matches 230; Conservative 0; Mismatches 46; Indels 8; Gaps 1;

Qy 1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
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Qy 1493 CCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGTCAGGTCACCGGCCCGGCAAGG 1552
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Db   758 CCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCGATCCGGCCAGAT 699

; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 5815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
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; PRIOR APPLICATION NUMBER: EP 04105484.2
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; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
;
; SEQ ID NO 195297
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-195297

Query Match   3.5%;   Score 184.2; DB 11; Length 1000;
Best Local Similarity 72.9%;   Pred. No. 7.5e-36;
Matches 237; Conservative   0; Mismatches 88; Indels   0; Gaps   0;

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Db   58 AGAGTCTTGTTCTGTCGTCACCCAGGCTGGGGTACGAGTGCGTGATCTCAACTCACTGCAACC 117

Qy   1340 TCTGCCTCCCAGGTCAAGCAATTCTCCTGCCTCCCGCGTAGCTCCAAGTAGCTGGGACTACAG 1399
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Db   118 TGTGCCTCCCAGGTTCAAGCGATTCTCACTTCTCCAGCCTTCCAAGTAGCTGGGACTACAG 177

Qy   1400 GCGCACGCGCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCG 1459
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 GTGCACGCGCTGGCTAATTTTTGTATTTTTTAGTAGAGAACGGAGTTTCCCCATACTGGCCA 237

Qy   1460 GCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAAGCCTCAGCCTCCTAAAGTGCTGGG 1519
            ||||||||||||||||||||||||||||||||||||||
Db   238 GCTGGTTTTGAACTCCTGACCTCAAGTGATCCACCCACCTCGGCGCCTCCGAAAGTGTTGGG 297

Qy   1520 ATTACAGGCATGAGTGAGCCACCGCGCCCGGCCCAAGGGTCAGTGTTTAATAAGGAATAACTTGA 1579
            ||||||||||||||||||||||||||||||||||||||||||||
Db   298 ATTACAGGCATGAGCCATGCACCCAGGTTCTGGGGTTCTTAACATGTATAATdCCA 357

Qy   1580 ATGGTTTACTAAACCAACAGGGAA 1604
            ||||||||||
Db   358 TGGATCCACACATGTAGCAACAAA 382

RESULT 5
US-10-868-184C-6721
; Sequence 6721, Application US/10868184C
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS805
; CURRENT APPLICATION NUMBER: US/10/868,184C
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US01/11988
; PRIOR FILING DATE: 2001-04-12

; PRIOR APPLICATION NUMBER: PCT/US00/06043
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06012
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06058
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06044
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06059
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06042
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06014
; PRIOR FILING DATE: 2000-03-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13046
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6721
; LENGTH: 17691
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-868-184C-6721

Query Match   3.5%;   Score 183.6; DB 6; Length 17691;
Best Local Similarity 78.2%;   Pred. No. 3.4e-35;
Matches 233; Conservative   0; Mismatches 64; Indels   1; Gaps   1;

Qy   1283 GTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCACACCTGAGCTCACTGCAACCTCT 1342
            || ||
Db   14938 GTCTCGCCTCTGTCGCCCAGGCGAGGAGTGCAATGCAGGACGATCTCAGCTCACTGCAACCTCT 14997

Qy   1343 GCCTCCCAGGTTCAAGCAATTCTCCTGCCTCCAGCCTCGGACTCAGTGGGACTACAGGCG 1402
            |||||||||||||||||||||||||||||||
Db   14998 GCCTCCCAGGTTCAAGCAATTCTCCTGTTTCAGCCTCCCGAGTAGCAGGGATTACAGGTG 15057

Qy   1403 CACGCCGGCTAA-TTTTGTATTGTTAGTAGAGATGGGGT 1461
            ||| |||||||||||||||||||
Db   15058 TGCGCCCAGCTAATTTTTTGTATTTTTTAGTAGAGACAGGGTTTCACCATGTTGGCCAGGC 15117

Qy   1462 TGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGGGAT 1521
            ||||||||||||||||||||||||||||||||||
Db   15118 TGGTCTTGAACTCCTGACCTCAAGTGATCCACCCTCCTCCGAAAGTGCTGCGGAT 15177

Qy   1522 TACAGGCATGAGTGAGCCACCGCGCCCGGCCCAAGGGTCAGTGTTTAATAAGGAATAACTTGA 1579
            || |||||||||||||||||||||||||||||
Db   15178 TATAGGCATGAGCCACCGCACCCGTGCTCGGCCAGAGGCCTTCTTTTAAGTGACTTCCAAGA 15235

RESULT 6
US-10-868-184C-6721
; Sequence 6721, Application US/10868184C
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS805
; CURRENT APPLICATION NUMBER: US/10/868,184C
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US01/11988
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US00/06043
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06012
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06058
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06044
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06059
; PRIOR FILING DATE: 2000-03-09

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; PRIOR APPLICATION NUMBER: PCT/US00/06042
; PRIOR APPLICATION FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06014
; PRIOR APPLICATION FILING DATE: 2000-03-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13046
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6721
; LENGTH: 17691
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-868-184C-6721

Query Match        3.5%;    Score 183.6;  DB 7;  Length 17691;
Best Local Similarity    78.2%;    Pred. No. 3.4e-35;
Matches 233;  Conservative  0;  Mismatches  64;  Indels  1;  Gaps  1;

Qy     1283 GTGAGGGCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCTCT 1342
            || | ||||||  ||||||| |||| |||||   ||||| ||||||| ||||||||||||
Db    14938 GTCTCGCTCGTGCCCAGGCAGGAGTGCAATGGCACGATCTCAGCTCACTGCAACCTCT 14997

Qy     1343 GCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGGTAGCTGGGACTACAGGCG 1402
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    14998 GCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGAGTAGCTGGGATTACAGGCG 15057

Qy     1403 CACGCCCCCGCTAA-TTTTTGTATTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCCGGC 1461
            ||||||||||| ||  ||||| |||||| |||||  |||||| |||||||||||||| ||| ||||||
Db    15058 TGCGCCCAGGCTAATTTTTGTATTTTTGTATTTTTAGTAGAGACAGGGTTTCACCATGTTGGCCAGGC 15117

Qy     1462 TGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCCAAAGTGCTGGGAT 1521
            |||||||||||||||||||||||||| ||| ||||||||||||||||||| |||||||||
Db    15118 TGGTCTTGAACTCCTGACCTCAGGTGATCCACCCTCCTCCACCTCCGAAAGTGCTGGGAT 15177

Qy     1522 TACAGGCGTGAGTGCACCGCGCCCGGCCCAAGGGTCAGTGTTTAATAAGGAATAACTTGA 1579
            || |||||||| ||||| ||||||| |||||| |||||||||| ||||||||||||||| |
Db    15178 TATAGGCATGAGCGCACCGCCGTCTCGGCCAGAGAGGCCTTCTTTAAGTGTGTGACTTCCAAGA 15235

RESULT 7
US-11-266-748A-212844
; Sequence 212844, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR APPLICATION FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR APPLICATION FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR APPLICATION FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR APPLICATION FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR APPLICATION FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR APPLICATION FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR APPLICATION FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR APPLICATION FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 212844
; LENGTH: 515
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-212844
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Query Match        3.5%;    Score 182.4;  DB 11;  Length 515;
Best Local Similarity    86.4%;    Pred. No. 1.6e-35;
Matches 216;  Conservative  0;  Mismatches  26;  Indels  8;  Gaps  1;

Qy     1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
            | ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db       46 ATCTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGCGGTTCAAGCGGATTCCTCCTGTCTCAGCCTCC 105

Qy     1381 CGCGTAGCTGGGACTACAGGCG-------CACGCGCCGGCTAATTTTTGTATTGTTAGTA 1432
            |||||||||||||  ||||||           ||||||||| |||||||||||||||||||
Db      106 CAAGTAGCTGGGATTACAGGCGCACACCACCACGCCCCGGCTAATTTTTGTATTTTTAGTA 165

Qy     1433 GAGATGGGGTTTCACCATATTAGCCCGTCTTGAACTCCTGACCTCAGGTGATCCA 1492
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db      166 GAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTCAGGTGATCCA 225

Qy     1493 CCCACCTCAGCCTCCTAAAGTGCTGGGATTACAGGCGATGAGTGCCGCGCCCGGCCCAAGG 1552
            ||||| |||||||| ||||| |||||||||||||||| |||||||  ||||| ||||||||
Db      226 CCCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGCCCACTGCCGCCCAGCCTAAT 285

Qy     1553 GTCAGTGTTT 1562
            ||  ||||||
Db      286 TTTTGTATTT 295

RESULT 8
US-11-266-748A-236144/c
; Sequence 236144, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR APPLICATION FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR APPLICATION FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR APPLICATION FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR APPLICATION FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR APPLICATION FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR APPLICATION FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR APPLICATION FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR APPLICATION FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 236144
; LENGTH: 515
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-236144

Query Match        3.5%;    Score 182.4;  DB 11;  Length 515;
Best Local Similarity    86.4%;    Pred. No. 1.6e-35;
Matches 216;  Conservative  0;  Mismatches  26;  Indels  8;  Gaps  1;

Qy     1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
            | ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db      470 ATCTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGCGGATTCCTCCTGTCTCAGCCTCC 411

Qy     1381 CGCGTAGCTGGGACTACAGGCG-------CACGCGCCGGCTAATTTTTGTATTGTTAGTA 1432
            |||||||||||||  ||||||           ||||||||| |||||||||||||||||||
Db      410 CAAGTAGCTGGGATTACAGGCGCACACCACCACGCCCCGGCTAATTTTTGTATTTTTAGTA 351
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Qy   1433 GAGATGGGGTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCA 1492
            |||||||||||||||||| ||||||||| ||||||| |||||||||||||||||||||
Db   350 GAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCA   291

Qy   1493 CCCACCTCAGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCGGCCAAGG   1552
            |||||||||||||||| | ||||||| |||||||||||||||||||||| ||||| -
Db   290 CCCACCTCGGCCCTCCCAAAGTGCTGGGATTACAGGCGCTGGGCCACTGCGCGCCCAGCCTAAT   231

Qy   1553 GTCAGGTGTT 1562
            || |||| |
Db   230 TTTTGTATTT   221

RESULT 9
US-11-266-748A-61740
; Sequence 61740, Application US/11266748A
; GENERAL INFORMATION:
;   APPLICANT: Harkin, Paul
;   APPLICANT: Johnston, Patrick
;   APPLICANT: Mulligan, Karl
;   TITLE OF INVENTION: Transcriptome Microarray Technology and
;   TITLE OF INVENTION: Methods of Using the Same
;   FILE REFERENCE: 55815-0102 (319189)
;   CURRENT APPLICATION NUMBER: US/11/266,748A
;   CURRENT FILING DATE: 2005-11-03
;   PRIOR APPLICATION NUMBER: EP 04105479.2
;   PRIOR FILING DATE: 2004-11-03
;   PRIOR APPLICATION NUMBER: EP 04105482.6
;   PRIOR FILING DATE: 2004-11-03
;   PRIOR APPLICATION NUMBER: EP 04105483.4
;   PRIOR FILING DATE: 2004-11-03
;   PRIOR APPLICATION NUMBER: EP 04105507.0
;   PRIOR FILING DATE: 2004-11-03
;   PRIOR APPLICATION NUMBER: EP 04105485.9
;   PRIOR FILING DATE: 2004-11-03
;   PRIOR APPLICATION NUMBER: EP 04105484.2
;   PRIOR FILING DATE: 2004-11-03
;   PRIOR APPLICATION NUMBER: US 60/662,276
;   PRIOR FILING DATE: 2005-03-14
;   PRIOR APPLICATION NUMBER: US 60/700,293
;   PRIOR FILING DATE: 2005-07-18
;   NUMBER OF SEQ ID NOS: 483996
;   SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61740
;   LENGTH: 101500
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-61740

Query Match   3.4%;   Score 180.8; DB 11; Length 101500;
Best Local Similarity 79.0%;   Pred. No. 3.4e-34;
Matches 215; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy   1281 GGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTGTATGCTCTACACCTGAGCTCACTGCAACCT 1340
            | ||| ||||| |||| || |||||||||||| ||||| |||||||| |||| ||||||||||||
Db   76041 GAGTCTCGCTCTCGTTGCCCAGGCTAGAGTGCAATGGCACGATCTTGGCTCATTGCAACCT 76100

Qy   1341 CTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCCTAGCTACAGG 1400
            | |||||||||||||||||||| ||||| ||| ||||||| |||| |||||||| |||
Db   76101 CGGCCCTCCCAGGTTCAAGCGATCCTCCTGCCTCAGCCTCCCAGTCACCCTAGTAGCTGGGATTACAGG 76160

Qy   1401 CGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCGG 1460
            | ||| || |||||||||| |||||| |||||||||||||| ||||||||||||||||
Db   76161 CATGCACCCGGCTAATTTTTGTATTTATTAGTAGAGACAGAGTTTCACCATGTTGGCCAGG 76220

Qy   1461 CTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCCTAAAGTGCTGGGA 1520
            |||||||| ||||||||||||||| |||||||||||||||| |||||||||||||
Db   76221 CTGGTCTCGAACTCCTGACCTCAGGTGATCCAGCCCACCTCCCAAAGTGCTGGGA 76280

Qy   1521 TTACAGGCATGAGTCACCGCGCCCGGCCAAGG 1552
            |||||||| |||||| ||||||||| ||||||
Db   76281 TTACAGGCGTGAGCCGTGAGCCACTGCGCCCGGCCCAAG 76312

RESULT 10
US-11-214-063A-1285
; Sequence 1285, Application US/11214063A
; GENERAL INFORMATION:
;   APPLICANT: SUWA, MAKIKO
;   APPLICANT: ASAI, KIYOSHI
;   APPLICANT: AKIYAMA, YUTAKA
;   APPLICANT: ABURATANI, HIROYUKI
;   TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
;   FILE REFERENCE: 084335/166
;   CURRENT APPLICATION NUMBER: US/11/214,063A
;   CURRENT FILING DATE: 2005-08-30
;   PRIOR APPLICATION NUMBER: US/10/292,798
;   PRIOR FILING DATE: 2002-11-13
;   PRIOR APPLICATION NUMBER: 10/017,161
;   PRIOR FILING DATE: 2001-12-18
;   PRIOR APPLICATION NUMBER: JP 2001-246789
;   PRIOR FILING DATE: 2001-06-18
;   NUMBER OF SEQ ID NOS: 2070
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1285
;   LENGTH: 39729
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   LOCATION: source
;   FEATURE:
;   LOCATION: (1)..(39729)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (201)..(409)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1705)..(1966)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (3861)..(4281)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (6128)..(6513)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (13450)..(13658)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (15064)..(15254)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (15941)..(16150)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (20045)..(20170)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (22124)..(22422)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (22512)..(22683)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (23437)..(23604)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (24073)..(24309)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (27352)..(27646)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (28263)..(28408)
;   FEATURE:

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; NAME/KEY:  CDS                              ; NAME/KEY:  CDS
; LOCATION:  (28910)..(29146)                 ; LOCATION:  (1011)..(1148)
; FEATURE:                                     ; FEATURE:
; NAME/KEY:  CDS                              ; NAME/KEY:  CDS
; LOCATION:  (30241)..(30380)                 ; LOCATION:  (1986)..(2325)
; FEATURE:                                     ; FEATURE:
; NAME/KEY:  CDS                              ; NAME/KEY:  CDS
; LOCATION:  (36370)..(36640)                 ; LOCATION:  (2353)..(2484)
; FEATURE:                                     ; FEATURE:
; NAME/KEY:  CDS                              ; NAME/KEY:  CDS
; LOCATION:  (36749)..(36992)                 ; LOCATION:  (2638)..(2820)
; FEATURE:                                     ; FEATURE:
; NAME/KEY:  CDS                              ; NAME/KEY:  CDS
; LOCATION:  (39268)..(39529)                 ; LOCATION:  (3675)..(3857)
US-11-214-063A-1285                           ; FEATURE:
                                              ; NAME/KEY:  CDS
Query Match          3.4%;    Score 180.6;     ; LOCATION:  (4320)..(4429)
DB 11;  Length 39729;                          ; FEATURE:
Best Local Similarity   81.2%;  Pred. No. 2.6e-34;  ; NAME/KEY:  CDS
Matches  225;  Conservative  0;  Mismatches  44;  Indels  8;  Gaps  1;   ; LOCATION:  (4632)..(4697)
                                              ; FEATURE:
Qy  1321  ACCTGAGCTCACTGCAACCTCTGCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380   ; NAME/KEY:  CDS
          | || ||||||||||||||||||||| ||||| |||||  |||||| ||||||||||||||  ; LOCATION:  (4867)..(4992)
Db 24907  ATCTCGGCTCACTGCAACCTCTGCTCCCAGGGTTCAATCGATTCTCCTGCCTCAGCCTCC 24966  ; FEATURE:
                                              ; NAME/KEY:  CDS
Qy  1381  CGCGTAGCTGGGACTACAGGCGCAC--------GCCCGGCTAATTTTGTATTGTTAGTA 1432   ; LOCATION:  (5152)..(5228)
          || |||||||||||| ||||| ||||         |||||||| |||| |||| ||||||  ; FEATURE:
Db 24967  CGAGTAGCTGGGATGACAGGTGCGCACCACCATGCCTGCTAATTTTGTATTTTTAGTA 25026  ; NAME/KEY:  CDS
                                              ; LOCATION:  (5316)..(5379)
Qy  1433  GAGATGGGGTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCA 1492   ; FEATURE:
          |||||||||||| |||||||| |||||| ||||||||||||||||||| ||||||||||||  ; NAME/KEY:  CDS
Db 25027  GAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCG 25086  ; LOCATION:  (5492)..(5577)
                                              ; FEATURE:
Qy  1493  CCCACCTCAGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGG 1552   ; NAME/KEY:  CDS
          |||||||||||||||| |||| |||||||||||||||| |||||||  ||||||| ||||  ; LOCATION:  (5753)..(5810)
Db 25087  CCCGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCCGCCCGGCCTGAG 25146  ; FEATURE:
                                              ; NAME/KEY:  CDS
Qy  1553  GTCAGTGTTTAATAAGGAATAACTTGAATGGTTTACT 1589  ; LOCATION:  (6327)..(6431)
          |||| ||  |||||  ||||| ||  |||||||||  ; FEATURE:
Db 25147  TTTTCCTTTTATGAAGGACCTGCTTGGTTGGTTGCCT 25183  ; NAME/KEY:  CDS
                                              ; LOCATION:  (7312)..(7406)
                                              ; FEATURE:
                                              ; NAME/KEY:  CDS
                                              ; LOCATION:  (7489)..(7557)
RESULT 11                                     ; FEATURE:
US-11-214-063A-1715                           ; NAME/KEY:  CDS
; Sequence 1715, Application US/11214063A     ; LOCATION:  (7741)..(7845)
; GENERAL INFORMATION:                         ; FEATURE:
; APPLICANT:  SUWA, MAKIKO                     ; NAME/KEY:  CDS
; APPLICANT:  ASAI, KIYOSHI                    ; LOCATION:  (9174)..(9447)
; APPLICANT:  AKIYAMA, YUTAKA                  ; FEATURE:
; APPLICANT:  ABURATANI, HIROYUKI              ; NAME/KEY:  CDS
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  ; LOCATION:  (10656)..(10748)
; FILE REFERENCE: 084335/166                   ; FEATURE:
; CURRENT APPLICATION NUMBER: US/11/214,063A   ; NAME/KEY:  modified_base
; CURRENT FILING DATE: 2005-08-30             ; LOCATION:  (6983)..77082)
; PRIOR APPLICATION NUMBER: US/10/292,798      ; OTHER INFORMATION: a, t, c, g, unknown or other
; PRIOR FILING DATE: 2002-11-13               ; FEATURE:
; PRIOR APPLICATION NUMBER: 10/017,161         ; NAME/KEY:  modified_base
; PRIOR FILING DATE: 2001-12-18               ; LOCATION:  (9991)..7991)
; PRIOR APPLICATION NUMBER: JP 2001-246789     ; OTHER INFORMATION: a, t, c, g, unknown or other
; PRIOR FILING DATE: 2001-06-18               ; FEATURE:
; NUMBER OF SEQ ID NOS: 2070                   ; NAME/KEY:  modified_base
; SOFTWARE:  PatentIn Ver. 2.1                 ; LOCATION:  (10873)..(10873)
SEQ ID NO 1715                                ; OTHER INFORMATION: a, t, c, g, unknown or other
; LENGTH: 10948                               US-11-214-063A-1715
; TYPE: DNA
; ORGANISM: Homo sapiens                      Query Match          3.4%;  Score 179.4;  DB 11;  Length 10948;
; FEATURE:                                     Best Local Similarity  78.0%;  Pred. No. 3.1e-34;
; NAME/KEY:  source                            Matches  216;  Conservative  0;  Mismatches  61;  Indels  0;  Gaps  0;
; LOCATION:  (1)..(10948)
; FEATURE:                                     Qy  1288  GGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACCTGCAACCCTGCCTC 1347
; NAME/KEY:  CDS                                         |||| |||||| ||||||||||||||||| |||||||| ||||||||||||||||||||
; LOCATION:  (201)..(572)
; FEATURE:
```

Db　　1481　GCTCCGTCACCCAGGCTGGAGTGGTAGTGGCGGATCTCAGCTCACTGCACCCTCTGCCTC　1540
　　　　　　　　　　　|||||| ||||| ||||||||||||||
Qy　　1348　CCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGGGCTAGCTGGGACTACAGGCGCACGC　1407

Qy　　1541　CTGGGGTTCAAACAATTCTCGTGTGCCTCCAGCCTCCCAAGTAGCTGGGATTACAGGTGTGTAC　1600
　　　　　　　　|||||| || ||||||||||||||||||||||
Db　　1408　CCGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATATTAGCCGGCTGGTCT　1467

Db　　1601　CCGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTAGTCT　1660

Qy　　1468　TGAACTCCTGACCTCAGGTGATCCACCCACCTCCTAAAGTGCTGGGATTACAGG　1527
　　　　　　　|||||| ||||||||||||||||| |||||
Db　　1661　TGAACTCCTGACCTCAGGTGACCCACCTGCCTCGGACTCCCAAAGTGCTGGGATTACAGG　1720

Qy　　1528　CATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTAA　1564
　　　　　　　|||||| ||||||||
Db　　1721　CATGAGCCACTGCACCAGACCCCACCTCAGTTTCTGA　1757

RESULT 12
US-10-868-184C-6360/c
; Sequence 6360, Application US/10868184C
; GENERAL INFORMATION:
;　APPLICANT: Rosen, et. al
;　TITLE OF INVENTION: Human Secreted Proteins
;　FILE REFERENCE: PS805
;　CURRENT APPLICATION NUMBER: US/10/868,184C
;　CURRENT FILING DATE: 2004-06-16
;　PRIOR APPLICATION NUMBER: 60/278,650
;　PRIOR FILING DATE: 2001-03-27
;　PRIOR APPLICATION NUMBER: 09/833,245
;　PRIOR FILING DATE: 2001-04-12
;　PRIOR APPLICATION NUMBER: PCT/US01/11988
;　PRIOR FILING DATE: 2001-04-12
;　PRIOR APPLICATION NUMBER: PCT/US00/06043
;　PRIOR FILING DATE: 2000-03-09
;　PRIOR APPLICATION NUMBER: PCT/US00/06012
;　PRIOR FILING DATE: 2000-03-09
;　PRIOR APPLICATION NUMBER: PCT/US00/06058
;　PRIOR FILING DATE: 2000-03-09
;　PRIOR APPLICATION NUMBER: PCT/US00/06044
;　PRIOR FILING DATE: 2000-03-09
;　PRIOR APPLICATION NUMBER: PCT/US00/06059
;　PRIOR FILING DATE: 2000-03-09
;　PRIOR APPLICATION NUMBER: PCT/US00/06042
;　PRIOR FILING DATE: 2000-03-09
;　PRIOR APPLICATION NUMBER: PCT/US00/06014
;　PRIOR FILING DATE: 2000-03-09
;　Remaining Prior Application data removed - See File Wrapper or PALM.
;　NUMBER OF SEQ ID NOS: 13046
;　SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6360
;　LENGTH: 6708
;　TYPE: DNA
;　ORGANISM: Homo sapiens
US-10-868-184C-6360

Query Match　　　　　3.4%;　　Score 179.2;　DB 6;　Length 6708;
Best Local Similarity　　77.9%;　Pred. No. 2.9e-34;
Matches　232;　Conservative　　0;　Mismatches　58;　Indels　8;　Gaps　1;

Qy　　1290　TCTGTGTCTTACACCTACCTGTATGCTCACACCTGAGCTCACTGCAACCTCTGCCTCCC　1349
　　　　　　　||||| ||||||||||| | |||||||||||||||||||||
Db　　3909　TCTGTCTCTCAGGCTGGAGTACAGTGCACAATCTCAGCTCACTGCAACCTCTGCCTCCC　3850

Qy　　1350　AGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGGGCTAGCTGGGACTACAGGCG------　1402
　　　　　　　|||||||||||||||||||||| ||||||||||||||||||
Db　　3849　AGGTTCAAGTAATTCTCCTGTCTCAGCCTCCCGAGTAGCTGGGATTACAGGTGCCCAACA　3790

Qy　　1403　-CACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCGGC　1461
　　　　　　　 |||| || |||||||| ||| |||||||||||||||||||
Db　　3789　CCACACATGGCTAATTTTTTGTATTTTTAGTAGAGATGGGGTTTGCCATGTTAGCCAGGC　3730

RESULT 14

US-10-868-184C-6360/c
; Sequence 6360, Application US/10868184C
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS805
; CURRENT APPLICATION NUMBER: US/10/868,184C
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US01/11988
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US00/06043
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06012
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06058
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06044
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06059
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06042
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06014
; PRIOR FILING DATE: 2000-03-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13046
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6360
; LENGTH: 6708
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-868-184C-6360

Query Match   3.4%;   Score 179.2; DB 7; Length 6708;
Best Local Similarity   77.9%;   Pred. No. 2.9e-34;
Matches 232; Conservative   0; Mismatches 58; Indels   8; Gaps   1;

Qy   1290 TCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCTCTGCCTCC 1349
                    | || || | | |||||||||||||||||||||||
Db   3909 TCTGTCTCTCAGGCTGGAGTACAGTGGCACAATCTCAGCTCACTGCAACCTCTGCCTCCC 3850

Qy   1350 AGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCTAGCTGGGACTACAGGCG-------- 1402
                    |||||||||| |||||||||||||||||||
Db   3849 AGGTTCAAGTAATTCTCCTGCCTCCCGAGTAGCGGGATTACAGGTGCCCAACA 3790

Qy   1403 -CACGCCCGGCTAATTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCCGGC 1461
                    || || |||||| | ||||||| | |||||||
Db   3789 CCACACATGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTTGCCATGTTAGCCAGGC 3730

Qy   1462 TGGTCTTGAACTCCTGACCTCAGGTGATCCACCACCTCAAAGTGCTGGGAT 1521
                    |||||||||||| ||||| ||||||||||
Db   3729 TGGTCTTGAACTCCTGACCTCAGATGATCCGCCCTGCCTCGGCCTCTCAAAGTGCTGGGAT 3670

Qy   1522 TACAGGCATGAGTCACCGCGCCCGGCC 1579
                    |||||||||||| || |||
Db   3669 TACAGGCATGAGCCATGGTACACCTTTACTGAGGAAACAATTCA 3612

RESULT 15
US-10-868-184C-11267/c
; Sequence 11267, Application US/10868184C
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS805
; CURRENT APPLICATION NUMBER: US/10/868,184C
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: 60/278,650
; PRIOR FILING DATE: 2001-03-27